Fig. 1

met ser lys asn thr

val ser ser ala arg phe arg lys val asp val asp

glu tyr asp glu asn lys phe val asp glu glu asp

gly gly asp gly gln ala gly pro asp glu gly glu

val asp ser cys leu arg gln gly asn met thr ala

ala leu gln ala ala leu lys asn pro pro ile asn

thr **arg** ser gln ala val lys asp arg ala gly ser

ile val leu lys val leu ile ser phe lys ala **gly**

asp ile glu lys ala val gln ser leu asp **arg** asn

gly val asp leu leu met lys tyr ile tyr lys gly

phe glu ser pro ser asp asn ser ser ala **val** leu

leu gln trp his glu lys ala leu ala ala gly gly

val gly ser ile val arg val leu thr ala arg lys

thr val

Fig. 2A (1/3)

```
ggtctgtgtg tgcgtgcgtg cgagtgagtg agtgtgtgca tatttttttt tctcttttct     60
ttctctctct ttttttttct tttgcaaaga aacagcagcg ccgccgccgc tccgccgagg    120
cgctgcgccc cccgggggcg ggaggcggag gaggcgggca gcggcggagg gaggggagcc    180
ggggaggggg gcgccgcgct gggagggagg cagcgcgcac ggtgcagccg ggccgggcgg    240
gaggc atg gcg ggg ccc ccg gcc cta ccc ccg ccg gag acg gcg gcg gcc     290
     Met Ala Gly Pro Pro Ala Leu Pro Pro Pro Glu Thr Ala Ala Ala
       1               5                  10                  15

gcc acc acg gcc gcg gcc gcc gcc tcg tcg tcc gcc gct tcc ccg cac      338
Ala Thr Thr Ala Ala Ala Ala Ala Ser Ser Ser Ala Ala Ser Pro His
                  20                  25                  30

tac caa gag tgg att ctg gac acc atc gac tcg ctg cgc tcg cgc aag      386
Tyr Gln Glu Trp Ile Leu Asp Thr Ile Asp Ser Leu Arg Ser Arg Lys
              35                  40                  45

gcg cgg ccg gac ctg gag cgc atc tgc cgg atg gtg cgg cgg cgg cac      434
Ala Arg Pro Asp Leu Glu Arg Ile Cys Arg Met Val Arg Arg Arg His
          50                  55                  60

ggc ccg gag ccg gag cgc acg cgc gcc gag ctc gag aaa ctg atc cag      482
Gly Pro Glu Pro Glu Arg Thr Arg Ala Glu Leu Glu Lys Leu Ile Gln
      65                  70                  75

cag cgc gcc gtg ctc cgg gtc agc tac aag ggg agc atc tcg tac cgc      530
Gln Arg Ala Val Leu Arg Val Ser Tyr Lys Gly Ser Ile Ser Tyr Arg
  80                  85                  90                  95

aac gcg gcg cgc gtc cag ccg ccc cgg cgc gga gcc acc ccg ccg gcc      578
Asn Ala Ala Arg Val Gln Pro Pro Arg Arg Gly Ala Thr Pro Pro Ala
                 100                 105                 110

ccg ccg cgc gcc ccc cgc ggg ggc ccc gcc gcc gcc gcc gcg ccg ccg      626
Pro Pro Arg Ala Pro Arg Gly Gly Pro Ala Ala Ala Ala Ala Pro Pro
             115                 120                 125

ccc acg ccc gcc ccg ccg ccg ccg ccc gcg ccc gtc gcc gcc gcc gcc      674
Pro Thr Pro Ala Pro Pro Pro Pro Pro Ala Pro Val Ala Ala Ala Ala
         130                 135                 140

gcc ccg gcc cgg gcg ccc cgc gcg gcc gcc gcc gcc gct gcc gcc aca      722
Ala Pro Ala Arg Ala Pro Arg Ala Ala Ala Ala Ala Ala Ala Ala Thr
     145                 150                 155

gcg ccc ccc tcg ccc ggc ccc gcg cag ccg ggc ccc cgc gcg cag cgg      770
Ala Pro Pro Ser Pro Gly Pro Ala Gln Pro Gly Pro Arg Ala Gln Arg
160                 165                 170                 175

gcc gcg ccc ctg gcc gcg ccg ccg ccc gcg ccc gcc gct ccc ccg gcg      818
Ala Ala Pro Leu Ala Ala Pro Pro Pro Ala Pro Ala Ala Pro Pro Ala
                 180                 185                 190
```

Fig. 2A (continued 2/3)

```
gcg gcg ccc ccg gcc ggc ccg cgc cgc gcc ccc ccg ccc gcc gcc gcc      866
Ala Ala Pro Pro Ala Gly Pro Arg Arg Ala Pro Pro Pro Ala Ala Ala
            195                 200                 205

gtc gcc gcc cgg gag tcg ccg ctg ccg ccg ccg cca cag ccg ccg gcg      914
Val Ala Ala Arg Glu Ser Pro Leu Pro Pro Pro Pro Gln Pro Pro Ala
        210                 215                 220

ccg cca cag cag cag cag cag ccg ccg ccg cca ccg ccg ccg cag cag      962
Pro Pro Gln Gln Gln Gln Gln Pro Pro Pro Pro Pro Pro Pro Gln Gln
    225                 230                 235

cca cag ccg ccg ccg gag ggg ggc gcg gcg cgg gcc ggc ggc ccg gcg     1010
Pro Gln Pro Pro Pro Glu Gly Gly Ala Ala Arg Ala Gly Gly Pro Ala
240                 245                 250                 255

cgg ccc gtg agc ctg cgg gaa gtc gtg cgc tac ctc ggg ggt agc agc     1058
Arg Pro Val Ser Leu Arg Glu Val Val Arg Tyr Leu Gly Gly Ser Ser
                260                 265                 270

ggc gct ggc ggc cgc ctg acc cgc ggc cgc gtg cag ggt ctg ctg gaa     1106
Gly Ala Gly Gly Arg Leu Thr Arg Gly Arg Val Gln Gly Leu Leu Glu
            275                 280                 285

gag gag gcg gcg gcg cgg ggc cgc ctg gag cgc acc cgt ctc gga gcg     1154
Glu Glu Ala Ala Ala Arg Gly Arg Leu Glu Arg Thr Arg Leu Gly Ala
        290                 295                 300

ctt gcg ctg ccc cgc ggg gac agg ccc gga cgg gcg cca ccg gcc gcc     1202
Leu Ala Leu Pro Arg Gly Asp Arg Pro Gly Arg Ala Pro Pro Ala Ala
    305                 310                 315

agc gcc cgc gcg gcg cgg aac aag aga gct ggc gag gag cga gtg ctt     1250
Ser Ala Arg Ala Ala Arg Asn Lys Arg Ala Gly Glu Glu Arg Val Leu
320                 325                 330                 335

gaa aag gag gag gag gag gag gag gag gaa gac gac gag gac gac gac     1298
Glu Lys Glu Glu Glu Glu Glu Glu Glu Glu Asp Asp Glu Asp Asp Asp
                340                 345                 350

gac gac gtc gtg tcc gag ggc tcg gag gtg ccc gag agc gat cgt ccc     1346
Asp Asp Val Val Ser Glu Gly Ser Glu Val Pro Glu Ser Asp Arg Pro
            355                 360                 365

gcg ggt gcg cag cat cac cag ctg aat ggc ggc gag cgc ggc ccg cag     1394
Ala Gly Ala Gln His His Gln Leu Asn Gly Gly Glu Arg Gly Pro Gln
        370                 375                 380

acc gcc aag gag cgg gcc aag gag tgg tcg ctg tgt ggc ccc cac cct     1442
Thr Ala Lys Glu Arg Ala Lys Glu Trp Ser Leu Cys Gly Pro His Pro
    385                 390                 395

ggc cag gag gaa ggg cgg ggg ccg gcc gcg ggc agt ggc acc cgc cag     1490
Gly Gln Glu Glu Gly Arg Gly Pro Ala Ala Gly Ser Gly Thr Arg Gln
400                 405                 410                 415
```

Fig. 2A (continued 3/3)

```
gtg ttc tcc atg gcg gcc ttg agt aag gag ggg gga tca gcc tct tcg      1538
Val Phe Ser Met Ala Ala Leu Ser Lys Glu Gly Gly Ser Ala Ser Ser
                420                 425                 430

acg acc ggg cct gac tcc ccg tcc ccg gtg cct ttg ccc ccc ggg aag      1586
Thr Thr Gly Pro Asp Ser Pro Ser Pro Val Pro Leu Pro Pro Gly Lys
            435                 440                 445

cca gcc ctc cca gga gcc gat ggg acc ccc ttt ggc tgc cct gcc ggg      1634
Pro Ala Leu Pro Gly Ala Asp Gly Thr Pro Phe Gly Cys Pro Ala Gly
        450                 455                 460

cgc aaa gag aag ccg gca gac ccc gtg gag tgg aca gtc atg gac gtc      1682
Arg Lys Glu Lys Pro Ala Asp Pro Val Glu Trp Thr Val Met Asp Val
    465                 470                 475

gtg gag tac ttc acc gag gcg ggc ttc cct gag caa gcc acg gct ttc      1730
Val Glu Tyr Phe Thr Glu Ala Gly Phe Pro Glu Gln Ala Thr Ala Phe
480                 485                 490                 495

cag gag cag gag atc gac ggc aag tcc ctg ctg ctc atg cag cgc acc      1778
Gln Glu Gln Glu Ile Asp Gly Lys Ser Leu Leu Leu Met Gln Arg Thr
                500                 505                 510

gat gtc ctc acc ggc ctg tcc atc cgc ctg ggg cca gcg ttg aaa atc      1826
Asp Val Leu Thr Gly Leu Ser Ile Arg Leu Gly Pro Ala Leu Lys Ile
            515                 520                 525

tat gag cac cat atc aag gtg ctg cag cag ggt cac ttc gag gac gat      1874
Tyr Glu His His Ile Lys Val Leu Gln Gln Gly His Phe Glu Asp Asp
        530                 535                 540

gac ccg gaa ggc ttc ctg gga t gagcacagag ccgccgcgcc ccttgtcccc       1926
Asp Pro Glu Gly Phe Leu Gly
    545                 550

accccaccc cgcctggacc cattcctgcc tccatgtcac ccaaggtgtc ccagaggcca     1986
ggagctggac tgggcaggcg aggggtgcgg acctaccctg attctggtag ggggcggggc    2046
cttgctgtgc tcattgctac ccccccaccc cgtgtgtgtc tctgcacctg cccccagcac    2106
acccctcccg gagcctggat gtcgcctggg actctggcct gctcattttg cccccagatc    2166
agccccctcc ctccctcctg tcccaggaca ttttttaaaa gaaaaaaagg aaaaaaaaaa    2226
attggggagg gggctgggaa ggtgccccaa gatcctcctc ggcccaacca ggtgtttatt    2286
cctatatata tatatatatg ttttgttctg cctgtttttc gtttttttggt gcgtggcctt   2346
tcttccctcc caccaccact catggcccca gccctgctcg ccctgtcggc gggagcagct    2406
gggaatggga ggagggtggg accttgggtc tgtctcccac cctctctccc gttggttctg    2466
ttgtcgctcc agctggctgt attgcttttt aatattgcac cgaagggttg tttttttttt    2526
tttaaataaa attttaaaaa aaggaaaaaa aaaaa                               2561
```

Fig. 2B

asp cys arg ser ser ser asn asn arg Xaa pro lys
gly gly ala ala arg ala gly gly pro ala arg pro
val ser leu arg glu val val arg tyr leu gly gly
ser ser gly ala gly gly arg leu thr arg gly arg
val gln gly leu leu glu glu glu ala ala ala arg
gly arg leu glu arg thr arg leu gly ala leu ala
leu pro arg gly asp arg pro gly arg ala pro pro
ala ala ser ala arg ala ala arg asn lys arg ala
gly glu glu arg val leu glu lys glu glu glu glu
glu glu glu glu asp asp glu asp asp asp asp asp
val val ser glu gly ser glu val pro glu ser asp
arg pro ala gly ala gln his his gln leu asn gly
gly glu arg gly pro gln thr ala lys glu arg ala
lys glu trp ser leu cys gly pro his pro gly gln
glu glu gly arg gly pro ala ala gly ser gly thr
arg gln val phe ser met ala ala leu ser lys glu
gly gly ser ala ser ser thr thr gly pro asp ser
pro ser pro val pro leu pro pro gly lys pro ala
leu pro gly ala asp gly thr pro phe gly cys pro
ala gly arg lys glu lys pro ala asp pro val glu
trp thr val met asp val val glu tyr phe thr glu
ala gly phe pro glu gln ala thr ala phe gln glu
gln glu ile asp gly lys ser leu leu leu met gln
arg thr asp val leu thr gly leu ser ile arg leu
gly pro ala leu lys ile tyr glu his his ile lys
val leu gln gln gly his phe glu asp asp asp pro
glu gly phe leu gly

Fig. 3

ala ser ala arg ala ala arg asn lys arg ala gly glu glu arg val leu glu lys glu glu glu glu **glu glu glu** glu asp **asp glu asp asp** asp asp **asp val** val ser glu gly ser glu val pro glu ser asp arg pro ala gly ala gln his his gln leu asn **gly** gly glu arg gly pro gln **thr** ala lys glu arg **ala** lys glu trp **ser leu** cys gly pro his **pro** gly gln **glu** glu gly arg gly pro ala **ala** gly ser gly thr arg gln val phe ser met ala ala **leu ser** lys glu gly gly **ser** ala ser **ser thr** thr gly pro asp ser pro ser pro val pro leu pro pro gly lys pro ala leu pro gly ala asp gly thr pro phe gly cys pro **ala** gly arg lys glu lys pro **ala** asp pro val glu trp thr val met asp val val glu tyr phe thr glu ala gly phe pro glu gln ala thr ala phe gln glu gln glu ile asp gly lys ser leu leu leu met gln arg thr asp val leu thr gly leu ser ile arg leu gly pro ala leu lys ile tyr glu his his ile lys val leu gln gln gly his phe glu asp asp asp pro **glu** gly phe leu gly

Fig. 4

thr arg leu gly ala leu ala

leu pro arg gly asp arg pro gly arg ala pro pro

ala ala ser ala arg ala ala arg asn lys arg ala

gly glu glu arg val leu glu lys glu glu glu glu

glu glu glu glu asp **asp glu asp asp** asp asp **asp**

val val ser glu gly ser glu val pro glu ser asp

arg pro ala gly ala gln his his gln leu asn **gly**

gly glu arg gly pro gln **thr** ala lys glu arg **ala**

lys glu trp **ser leu** cys gly pro his **pro** gly gln

glu glu gly arg gly pro ala **ala** gly ser gly thr

arg gln val phe ser met ala ala **leu ser** lys glu

gly gly **ser** ala ser **ser thr** thr gly pro asp ser

pro ser pro val pro leu pro pro gly lys pro ala

leu pro gly ala asp gly thr pro phe gly cys pro

ala gly arg lys glu lys pro **ala** asp pro val glu

trp thr val met asp val val glu tyr phe thr glu

ala gly phe pro glu gln ala thr ala phe gln glu

gln glu ile asp gly lys ser leu leu leu met gln

arg thr asp val leu thr gly leu ser ile arg leu

gly pro ala leu lys ile tyr glu his his ile lys

val leu gln gln gly his phe glu asp asp asp pro

glu gly phe leu gly

Fig. 5

met lys asn gln
asp lys lys asn gly ala ala lys gln pro asn pro
lys ser ser pro gly gln pro glu ala gly **ala** glu
gly ala gln **gly** arg pro **gly** **arg** **pro** ala pro ala
arg glu ala glu gly **ala** ser ser gln ala pro **gly**
arg pro glu gly ala gln ala **lys** thr ala gln **pro**
gly ala leu **cys** asp val ser glu glu leu ser arg
gln leu glu asp ile leu ser thr tyr cys val asp
asn asn gln gly **ala** pro gly glu asp gly **val** gln
gly glu pro **pro** glu pro glu asp ala glu lys ser
arg **ala** tyr val ala arg asn gly glu pro glu pro
gly thr pro val val **asn** gly glu lys glu **thr** ser
lys **ala** **glu** pro **gly** thr glu glu ile arg **thr** ser
asp glu val gly asp arg asp his arg arg pro gln
glu lys lys lys ala lys gly leu gly lys glu ile
thr leu leu met gln thr leu asn thr leu ser thr
pro glu glu lys leu ala ala leu cys lys lys tyr
ala glu leu leu glu glu his arg asn ser gln lys
gln met lys leu leu gln lys lys gln ser gln leu
val gln glu lys asp his leu arg gly glu his ser
lys ala **ile** leu ala arg ser lys leu glu ser leu
cys arg glu leu gln arg his asn arg ser leu lys
glu glu gly val gln arg ala arg glu glu glu glu
lys arg lys glu val thr ser his phe gln **met** thr
leu asn asp ile gln leu gln met glu gln his asn
glu arg asn ser lys leu arg gln glu asn met glu

Fig. 5 (continued)

leu ala glu arg leu lys lys leu ile glu gln tyr
glu leu arg glu glu his ile asp lys val phe lys
his lys asp leu gln gln gln leu val asp ala lys
leu gln gln ala gln glu met leu lys glu ala glu
glu arg his gln arg glu lys asp phe leu leu lys
glu ala val glu ser gln arg met cys glu leu met
lys gln gln glu thr his leu lys gln gln leu ala
leu tyr thr glu lys phe glu glu phe gln asn thr
leu ser lys ser ser glu val phe thr thr phe lys
gln glu met glu lys met thr lys lys ile lys lys
leu glu lys glu thr thr met tyr arg ser arg trp
glu ser ser asn lys ala leu leu glu met ala glu
glu lys thr **leu** arg asp lys glu leu glu gly leu
gln val lys ile gln arg leu glu lys leu cys arg
ala leu gln thr glu arg asn asp leu asn lys arg
val gln asp leu ser ala gly gly gln gly **pro val**
ser asp ser gly pro glu arg arg pro **glu pro ala**
thr thr ser lys glu gln gly val glu gly pro gly
ala gln **val** pro **asn** ser pro arg **ala** thr **asp** ala
ser cys **cys ala** gly ala pro ser thr glu ala ser
gly gln thr gly pro gln glu pro thr **thr** ala **thr**
ala

Fig. 6

met ser lys asn thr val ser ser ala
arg phe arg lys val asp val asp glu tyr asp glu
asn lys phe val asp glu glu asp gly gly asp gly
gln ala gly pro asp glu gly glu val asp ser cys
leu arg gln gly asn met thr ala ala leu gln ala
ala leu lys asn pro pro ile asn thr **lys** ser gln
ala val lys asp arg ala gly ser ile val leu lys
val leu ile ser phe lys ala **asn** asp ile glu lys
ala val gln ser leu asp **lys** asn gly val asp leu
leu met lys tyr ile tyr lys gly phe glu ser pro
ser asp asn ser ser ala **met** leu leu gln trp his
glu lys ala leu ala ala gly gly val gly ser ile
val arg val leu thr ala arg lys thr val

Fig. 7A (1/3)

```
atg gcg ggg ccc ccg gcc cta ccc ccg ccg gag acg gcg gcg gcc gcc        48
Met Ala Gly Pro Pro Ala Leu Pro Pro Pro Glu Thr Ala Ala Ala Ala
 1               5                  10                  15

acc acg gcg gcc gcc gcc tcg tcg tcc gcc gct tcc ccg cac tac caa        96
Thr Thr Ala Ala Ala Ala Ser Ser Ser Ala Ala Ser Pro His Tyr Gln
            20                  25                  30

gag tgg atc ctg gac acc atc gac tcg ctg cgc tcg cgc aag gcg cgg       144
Glu Trp Ile Leu Asp Thr Ile Asp Ser Leu Arg Ser Arg Lys Ala Arg
        35                  40                  45

ccg gac ctg gag cgc atc tgc cgg atg gtg cgg cgg cgg cac ggc ccg       192
Pro Asp Leu Glu Arg Ile Cys Arg Met Val Arg Arg Arg His Gly Pro
    50                  55                  60

gag ccg gag cgc acg cgc gcc gag ctc gag aaa ctg atc cag cag cgc       240
Glu Pro Glu Arg Thr Arg Ala Glu Leu Glu Lys Leu Ile Gln Gln Arg
65                  70                  75                  80

gcc gtg ctc cgg gtc agc tac aag ggg agc atc tcg tac cgc aac gcg       288
Ala Val Leu Arg Val Ser Tyr Lys Gly Ser Ile Ser Tyr Arg Asn Ala
                85                  90                  95

gcg cgc gtc cag ccg ccc cgg cgc gga gcc acc ccg ccg gcc ccg ccg       336
Ala Arg Val Gln Pro Pro Arg Arg Gly Ala Thr Pro Pro Ala Pro Pro
            100                 105                 110

cgc gcc ccc cgc ggg gcc ccc gcc gcc gcc gcc gcc gcc gcg ccg ccg       384
Arg Ala Pro Arg Gly Ala Pro Ala Ala Ala Ala Ala Ala Ala Pro Pro
        115                 120                 125

ccc acg ccc gcc ccg ccg cca ccg ccc gcg ccc gtc gcc gcc gcc gcc       432
Pro Thr Pro Ala Pro Pro Pro Pro Pro Ala Pro Val Ala Ala Ala Ala
    130                 135                 140

ccg gcc cgg gcg ccc cgc gcg gcc gcc gcc gcc gcc gcc aca gcg ccc ccc       480
Pro Ala Arg Ala Pro Arg Ala Ala Ala Ala Ala Ala Thr Ala Pro Pro
145                 150                 155                 160

tcg cct ggc ccc gcg cag ccg ggc ccc cgc gcg cag cgg gcc gcg ccc       528
Ser Pro Gly Pro Ala Gln Pro Gly Pro Arg Ala Gln Arg Ala Ala Pro
                165                 170                 175

ctg gcc gcg ccg ccg ccc gcg cca gcc gct ccc ccg gcg gtg gcg ccc       576
Leu Ala Ala Pro Pro Pro Ala Pro Ala Ala Pro Pro Ala Val Ala Pro
            180                 185                 190

ccg gcc ggc ccg cgc cgc gcc ccc ccg ccc gcc gtc gcc gcc cgg gag       624
Pro Ala Gly Pro Arg Arg Ala Pro Pro Pro Ala Val Ala Ala Arg Glu
        195                 200                 205

ccg ccg ctg ccg ccg ccg cca cag ccg ccg gcg ccg cca cag cag cag       672
Pro Pro Leu Pro Pro Pro Pro Gln Pro Pro Ala Pro Pro Gln Gln Gln
    210                 215                 220
```

Fig. 7A (continued; 2/3)

```
cag ccg ccg ccg ccg cag cca cag ccg ccg ccg gag ggg ggc gcg gtg      720
Gln Pro Pro Pro Pro Gln Pro Gln Pro Pro Pro Glu Gly Gly Ala Val
225                 230                 235                 240

cgg gcc ggc ggc gcg gcg cgg ccc gtg agc ctg cgg gaa gtc gtg cgc      768
Arg Ala Gly Gly Ala Ala Arg Pro Val Ser Leu Arg Glu Val Val Arg
                245                 250                 255

tac ctc ggg ggc agc ggc ggc gcc ggc ggt cgc cta acc cgc ggc cgc      816
Tyr Leu Gly Gly Ser Gly Gly Ala Gly Gly Arg Leu Thr Arg Gly Arg
            260                 265                 270

gtg cag ggg ctg ctg gag gag gag gcg gcg gct cga ggc cgt ctg gag      864
Val Gln Gly Leu Leu Glu Glu Glu Ala Ala Ala Arg Gly Arg Leu Glu
        275                 280                 285

cgc acc cgt ctc gga gcg ctt gcg ctg ccc cgc ggg gac agg ccc gga      912
Arg Thr Arg Leu Gly Ala Leu Ala Leu Pro Arg Gly Asp Arg Pro Gly
    290                 295                 300

cgg gcg ccg ccg gcc gcc agc gcc cgc ccg tct cgc agc aag aga ggt      960
Arg Ala Pro Pro Ala Ala Ser Ala Arg Pro Ser Arg Ser Lys Arg Gly
305                 310                 315                 320

gga gaa gag cga gta ctt gag aaa gaa gag gaa gaa gat gat gat gaa     1008
Gly Glu Glu Arg Val Leu Glu Lys Glu Glu Glu Glu Asp Asp Asp Glu
                325                 330                 335

gat gaa gat gaa gaa gat gat gtg tca gag ggc tct gaa gtg ccc gag     1056
Asp Glu Asp Glu Glu Asp Asp Val Ser Glu Gly Ser Glu Val Pro Glu
            340                 345                 350

agt gac cgt cct gca ggt gcc cag cac cac cag ctt aac ggc gag cgg     1104
Ser Asp Arg Pro Ala Gly Ala Gln His His Gln Leu Asn Gly Glu Arg
        355                 360                 365

gga cct cag agt gcc aag gag agg gtc aag gag tgg acc ccc tgc gga     1152
Gly Pro Gln Ser Ala Lys Glu Arg Val Lys Glu Trp Thr Pro Cys Gly
    370                 375                 380

ccg cac cag ggc cag gat gaa ggg cgg ggg cca gcc ccg ggc agc ggc     1200
Pro His Gln Gly Gln Asp Glu Gly Arg Gly Pro Ala Pro Gly Ser Gly
385                 390                 395                 400

acc cgc cag gtg ttc tcc atg gca gcc atg aac aag gaa ggg gga aca     1248
Thr Arg Gln Val Phe Ser Met Ala Ala Met Asn Lys Glu Gly Gly Thr
                405                 410                 415

gct tct gtt gcc acc ggg cca gac tcc ccg tcc ccc gtg cct ttg ccc     1296
Ala Ser Val Ala Thr Gly Pro Asp Ser Pro Ser Pro Val Pro Leu Pro
            420                 425                 430

cca ggc aaa cca gcc cta cct ggg gcc gac ggg acc ccc ttt ggc tgt     1344
Pro Gly Lys Pro Ala Leu Pro Gly Ala Asp Gly Thr Pro Phe Gly Cys
        435                 440                 445
```

Fig. 7A (continued; 3/3)

```
ccg ccc ggg cgc aaa gag aag cca tct gat ccc gtc gag tgg acc gtg     1392
Pro Pro Gly Arg Lys Glu Lys Pro Ser Asp Pro Val Glu Trp Thr Val
    450                 455                 460

atg gat gtc gtc gaa tat ttt act gag gct gga ttc ccg gag cag gcg     1440
Met Asp Val Val Glu Tyr Phe Thr Glu Ala Gly Phe Pro Glu Gln Ala
465                 470                 475                 480

aca gct ttc caa gag cag gaa att gat ggc aaa tct ttg ctg ctc atg     1488
Thr Ala Phe Gln Glu Gln Glu Ile Asp Gly Lys Ser Leu Leu Leu Met
                485                 490                 495

cag cgc aca gat gtg ctc acc ggc ctg tcc atc cgc ctc ggg cca gcc     1536
Gln Arg Thr Asp Val Leu Thr Gly Leu Ser Ile Arg Leu Gly Pro Ala
            500                 505                 510

ctg aaa atc tac gag cac cac atc aag gtg ctt cag caa ggc cac ttt     1584
Leu Lys Ile Tyr Glu His His Ile Lys Val Leu Gln Gln Gly His Phe
        515                 520                 525

gag gat gat gac ccc gat ggc ttc tta ggc                            1614
Glu Asp Asp Asp Pro Asp Gly Phe Leu Gly
    530                 535
```

Fig. 7B

glu glu arg val leu glu lys glu glu glu glu **asp**

asp asp glu asp **glu asp glu glu** asp asp val ser

glu gly ser glu val pro glu ser asp arg pro ala

gly ala gln his his gln leu asn gly glu arg gly

pro gln **ser** ala lys glu arg **val** lys glu trp **thr**

pro cys gly pro his **gln** gly gln **asp** glu gly arg

gly pro ala **pro** gly ser gly thr arg gln val phe

ser met ala ala **met asn** lys glu gly gly **thr** ala

ser **val ala** thr gly pro asp ser pro ser pro val

pro leu pro pro gly lys pro ala leu pro gly ala

asp gly thr pro phe gly cys pro **pro** gly arg lys

glu lys pro **ser** asp pro val glu trp thr val met

asp val val glu tyr phe thr glu ala gly phe pro

glu gln ala thr ala phe gln glu gln glu ile asp

gly lys ser leu leu leu met gln arg thr asp val

leu thr gly leu ser ile arg leu gly pro ala leu

lys ile tyr glu his his ile lys val leu gln gln

gly his phe glu asp asp asp pro **asp** gly phe leu

gly

Fig. 8A (1/3)

```
atg aag aac caa gac aaa aag aac ggg gct gcc aaa caa tcc aat cca       48
Met Lys Asn Gln Asp Lys Lys Asn Gly Ala Ala Lys Gln Ser Asn Pro
 1               5                  10                  15

aaa agc agc cca gga caa ccg gaa gca gga ccc gag gga gcc cag gag       96
Lys Ser Ser Pro Gly Gln Pro Glu Ala Gly Pro Glu Gly Ala Gln Glu
            20                  25                  30

cgg ccc agc cag gcg gct cct gca gta gaa gca gaa ggt ccc ggc agc      144
Arg Pro Ser Gln Ala Ala Pro Ala Val Glu Ala Glu Gly Pro Gly Ser
        35                  40                  45

agc cag gct cct cgg aag ccg gag ggt gct caa gcc aga acg gct cag      192
Ser Gln Ala Pro Arg Lys Pro Glu Gly Ala Gln Ala Arg Thr Ala Gln
    50                  55                  60

tct ggg gcc ctt cgt gat gtc tct gag gag ctg agc cgc caa ctg gaa      240
Ser Gly Ala Leu Arg Asp Val Ser Glu Glu Leu Ser Arg Gln Leu Glu
65                  70                  75                  80

gac ata ctg agc aca tac tgt gtg gac aat aac cag ggg ggc ccc ggc      288
Asp Ile Leu Ser Thr Tyr Cys Val Asp Asn Asn Gln Gly Gly Pro Gly
                85                  90                  95

gag gat ggg gca cag ggt gag ccg gct gaa ccc gaa gat gca gag aag      336
Glu Asp Gly Ala Gln Gly Glu Pro Ala Glu Pro Glu Asp Ala Glu Lys
            100                 105                 110

tcc cgg acc tat gtg gca agg aat ggg gag cct gaa cca act cca gta      384
Ser Arg Thr Tyr Val Ala Arg Asn Gly Glu Pro Glu Pro Thr Pro Val
        115                 120                 125

gtc aat gga gag aag gaa ccc tcc aag ggg gat cca aac aca gaa gag      432
Val Asn Gly Glu Lys Glu Pro Ser Lys Gly Asp Pro Asn Thr Glu Glu
    130                 135                 140

atc cgg cag agt gac gag gtc gga gac cga gac cat cga agg cca cag      480
Ile Arg Gln Ser Asp Glu Val Gly Asp Arg Asp His Arg Arg Pro Gln
145                 150                 155                 160

gag aag aaa aaa gcc aag ggt ttg ggt aag gag atc acg ttg ctg atg      528
Glu Lys Lys Lys Ala Lys Gly Leu Gly Lys Glu Ile Thr Leu Leu Met
                165                 170                 175

cag aca ttg aat act ctg agt acc cca gag gag aag ctg gct gct ctg      576
Gln Thr Leu Asn Thr Leu Ser Thr Pro Glu Glu Lys Leu Ala Ala Leu
            180                 185                 190

tgc aag aag tat gct gaa ctg ctg gag gag cac cgg aat tca cag aag      624
Cys Lys Lys Tyr Ala Glu Leu Leu Glu Glu His Arg Asn Ser Gln Lys
        195                 200                 205
```

Fig. 8A (continued; 2/3)

```
cag atg aag ctc cta cag aaa aag cag agc cag ctg gtg caa gag aag      672
Gln Met Lys Leu Leu Gln Lys Lys Gln Ser Gln Leu Val Gln Glu Lys
    210                 215                 220

gac cac ctg cgc ggt gag cac agc aag gcc gtc ctg gcc cgc agc aag      720
Asp His Leu Arg Gly Glu His Ser Lys Ala Val Leu Ala Arg Ser Lys
225                 230                 235                 240

ctt gag agc cta tgc cgt gag ctg cag cgg cac aac cgc tcc ctc aag      768
Leu Glu Ser Leu Cys Arg Glu Leu Gln Arg His Asn Arg Ser Leu Lys
                245                 250                 255

gaa gaa ggt gtg cag cgg gcc cgg gag gag gag gag aag cgc aag gag      816
Glu Glu Gly Val Gln Arg Ala Arg Glu Glu Glu Glu Lys Arg Lys Glu
            260                 265                 270

gtg acc tcg cac ttc cag gtg aca ctg aat gac att cag ctg cag atg      864
Val Thr Ser His Phe Gln Val Thr Leu Asn Asp Ile Gln Leu Gln Met
        275                 280                 285

gaa cag cac aat gag cgc aac tcc aag ctg cgc caa gag aac atg gag      912
Glu Gln His Asn Glu Arg Asn Ser Lys Leu Arg Gln Glu Asn Met Glu
    290                 295                 300

ctg gct gag agg ctc aag aag ctg att gag cag tat gag ctg cgc gag      960
Leu Ala Glu Arg Leu Lys Lys Leu Ile Glu Gln Tyr Glu Leu Arg Glu
305                 310                 315                 320

gag cat atc gac aaa gtc ttc aaa cac aag gac cta caa cag cag ctg     1008
Glu His Ile Asp Lys Val Phe Lys His Lys Asp Leu Gln Gln Gln Leu
                325                 330                 335

gtg gat gcc aag ctc cag cag gcc cag gag atg cta aag gag gca gaa     1056
Val Asp Ala Lys Leu Gln Gln Ala Gln Glu Met Leu Lys Glu Ala Glu
            340                 345                 350

gag cgg cac cag cgg gag aag gat ttt ctc ctg aaa gag gca gta gag     1104
Glu Arg His Gln Arg Glu Lys Asp Phe Leu Leu Lys Glu Ala Val Glu
        355                 360                 365

tcc cag agg atg tgt gag ctg atg aag cag caa gag acc cac ctg aag     1152
Ser Gln Arg Met Cys Glu Leu Met Lys Gln Gln Glu Thr His Leu Lys
    370                 375                 380

caa cag ctt gcc cta tac aca gag aag ttt gag gag ttc cag aac aca     1200
Gln Gln Leu Ala Leu Tyr Thr Glu Lys Phe Glu Glu Phe Gln Asn Thr
385                 390                 395                 400

ctt tcc aaa agc agc gag gta ttc acc aca ttc aag cag gag atg gaa     1248
Leu Ser Lys Ser Ser Glu Val Phe Thr Thr Phe Lys Gln Glu Met Glu
                405                 410                 415
```

Fig. 8A (continued; 3/3)

```
aag atg act aag aag atc aag aag ctg gag aaa gaa acc acc atg tac     1296
Lys Met Thr Lys Lys Ile Lys Lys Leu Glu Lys Glu Thr Thr Met Tyr
            420                 425                 430

cgg tcc cgg tgg gag agc agc aac aag gcc ctg ctt gag atg gct gag     1344
Arg Ser Arg Trp Glu Ser Ser Asn Lys Ala Leu Leu Glu Met Ala Glu
        435                 440                 445

gag aaa aca gtc cgg gat aaa gaa ctg gag ggc ctg cag gta aaa atc     1392
Glu Lys Thr Val Arg Asp Lys Glu Leu Glu Gly Leu Gln Val Lys Ile
    450                 455                 460

caa cgg ctg gag aag ctg tgc cgg gca ctg cag aca gag cgc aat gac     1440
Gln Arg Leu Glu Lys Leu Cys Arg Ala Leu Gln Thr Glu Arg Asn Asp
465                 470                 475                 480

ctg aac aag agg gta cag gac ctg agt gct ggt ggc cag ggc tcc ctc     1488
Leu Asn Lys Arg Val Gln Asp Leu Ser Ala Gly Gly Gln Gly Ser Leu
                485                 490                 495

act gac agt ggc cct gag agg agg cca gag ggg cct ggg gct caa gca     1536
Thr Asp Ser Gly Pro Glu Arg Arg Pro Glu Gly Pro Gly Ala Gln Ala
            500                 505                 510

ccc agc tcc ccc agg gtc aca gaa gcg cct tgc tac cca gga gca ccg     1584
Pro Ser Ser Pro Arg Val Thr Glu Ala Pro Cys Tyr Pro Gly Ala Pro
        515                 520                 525

agc aca gaa gca tca ggc cag act ggg cct caa gag ccc acc tcc gcc     1632
Ser Thr Glu Ala Ser Gly Gln Thr Gly Pro Gln Glu Pro Thr Ser Ala
    530                 535                 540

agg gcc                                                            1638
Arg Ala
545
```

Fig. 8 B

lys ser ser pro gly gln pro glu ala gly **pro** glu gly ala gln **glu** arg pro **ser** **gln** **ala** ala pro ala **val** glu ala glu gly **pro** **gly** ser ser gln ala pro **arg** **lys** pro glu gly ala gln ala **arg** thr ala gln **ser** gly ala leu **arg** asp val ser glu glu leu ser arg gln leu glu asp ile leu ser thr tyr cys val asp asn asn gln gly **gly** pro gly glu asp gly **ala** gln gly glu pro **ala** glu pro glu asp ala glu lys ser arg **thr** tyr val ala arg asn gly glu pro glu pro thr pro val val **tyr** gly glu lys glu **pro** ser lys **gly** **asp** pro **asn** thr glu glu ile arg **gln** ser asp glu val gly asp arg asp his arg arg pro gln glu lys lys lys ala lys gly leu gly lys glu ile thr leu leu met gln thr leu asn thr leu ser thr pro glu glu lys leu ala ala leu cys lys lys tyr ala glu leu leu glu glu his arg asn ser gln lys gln met lys leu leu gln lys lys gln ser gln leu val gln glu lys asp his leu arg gly glu his ser lys ala **val** leu ala arg ser lys leu glu ser leu cys arg glu leu gln arg his asn arg ser leu lys glu glu gly val gln arg ala arg glu glu glu glu lys arg lys glu val thr ser his phe gln **val** thr leu asn asp ile gln leu gln met glu gln his asn glu arg asn ser lys leu arg gln glu asn met glu leu ala glu arg leu lys lys leu ile glu gln tyr glu leu arg glu glu his ile asp lys val phe lys his lys asp leu gln gln gln leu val asp ala lys leu gln gln ala gln glu met leu lys glu ala glu glu arg his gln arg glu lys asp phe leu leu lys glu ala val glu ser gln arg met cys glu leu met lys gln gln glu thr his leu lys gln gln leu ala leu tyr thr glu lys phe glu glu phe gln asn thr leu ser lys ser ser

Fig. 8 B(continued)

glu val phe thr thr phe lys gln glu met glu lys met thr lys
lys ile lys lys leu glu lys glu thr thr met tyr arg ser arg
trp glu ser ser asn lys ala leu leu glu met ala glu glu lys
thr **val** arg asp lys glu leu glu gly leu gln val lys ile gln
arg leu glu lys leu cys arg ala leu gln thr glu arg asn asp
leu asn lys arg val gln asp leu ser ala gly gly gln gly **ser**
leu thr asp ser gly pro glu arg arg pro glu gly pro gly ala
gln **ala** pro **ser** ser pro arg **val** thr **glu** ala **pro** cys **tyr pro**
gly ala pro ser thr glu ala ser gly gln thr gly pro gln glu
pro thr **ser** ala **arg** ala ***

Fig. 9

val asp val asp

glu tyr asp glu asn lys phe val asp glu glu asp

gly gly asp gly

Fig. 10

1	AAG	CCT	CGC	AGC	GGT	CGG	GGC	GGC	GCC	GCG	GAG	GCT
37	CGA	GGG	CGG	CGG	GCG	GCG	GCG	ATG	TCG	AAG	AAC	ACG
								met	ser	lys	asn	thr
73	GTG	TCG	TCG	GCG	CGG	TTC	CGG	AAG	GTG	GAC	GTG	GAT
	val	ser	ser	ala	arg	phe	arg	lys	val	asp	val	asp
109	GAG	TAC	GAC	GAG	AAC	AAG	TTC	GTG	GAC	GAG	GAA	GAC
	glu	tyr	asp	glu	asn	lys	phe	val	asp	glu	glu	asp
145	GGC	GGC	GAC	GGC	CAG	GCG	GGG	CCG	GAC	GAG	GGC	GAG
	gly	gly	asp	gly	gln	ala	gly	pro	asp	glu	gly	glu
181	GTG	GAC	TCG	TGC	CTG	CGG	CAA	GGG	AAC	ATG	ACA	GCC
	val	asp	ser	cys	leu	arg	gln	gly	asn	met	thr	ala
217	GCC	CTG	CAG	GCG	GCG	CTG	AAG	AAC	CCT	CCC	ATC	AAC
	ala	leu	gln	ala	ala	leu	lys	asn	pro	pro	ile	asn
253	ACC	AGG	AGC	CAG	GCG	GTG	AAG	GAC	CGG	GCA	GGC	AGC
	thr	**arg**	ser	gln	ala	val	lys	asp	arg	ala	gly	ser
289	ATC	GTG	CTG	AAG	GTG	CTC	ATC	TCC	TTC	AAG	GCC	GGC
	ile	val	leu	lys	val	leu	ile	ser	phe	lys	ala	**gly**
325	GAC	ATA	GAA	AAG	GCC	GTG	CAG	TCC	CTG	GAC	AGG	AAC
	asp	ile	glu	lys	ala	val	gln	ser	leu	asp	**arg**	asn
361	GGC	GTG	GAC	CTG	CTC	ATG	AAG	TAC	ATC	TAC	AAG	GGC
	gly	val	asp	leu	leu	met	lys	tyr	ile	tyr	lys	gly
397	TTC	GAG	AGC	CCC	TCC	GAC	AAC	AGC	AGC	GCC	GTG	CTC
	phe	glu	ser	pro	ser	asp	asn	ser	ser	ala	**val**	leu
433	CTG	CAG	TGG	CAC	GAG	AAG	GCG	CTG	GCT	GCA	GGA	GGA
	leu	gln	trp	his	glu	lys	ala	leu	ala	ala	gly	gly
469	GTG	GGC	TCC	ATC	GTC	CGT	GTC	CTG	ACT	GCA	AGG	AAA
	val	gly	ser	ile	val	arg	val	leu	thr	ala	arg	lys
505	ACC	GTG	TAG	CCT	GGC	AGG	AAC	GGG	TGC	CTG	CCG	GGG
	thr	val										

Fig. 10 (continued)

```
 541  AGC GGG AGC TGC CGG TAC AAA GAC CAA AAC GCC CAG
 577  ATG CCG CCG CTG CCC TGT GGG CGG CGT CTG TTC CCA
 613  GCT TCG CTT TTT CCC TTT CCC GTG TCT GTC AGG ATT
 649  ACA TAA GGT TTC CCT TCG TGA GAA TCG GAG TGG CGC
 685  AGA GGG TCC TGT TCA TAC GCG CCG TGC GTC CGG CTG
 721  TGT AAG ACC CCT GCC TTC AGT GTC CTT GAG CAA CGG
 757  TAG CGT GTC GCC GGC TGG GTT TGG TTT TGT CGT GGA
 793  GGG ATC TGG TCA GAA TTT GAG GCC AGT TTC CTA ACT
 829  CAT TGC TGG TCA GGA AAT GAT CTT CAT TTA AAA AAA
 865  AAA AAA AGA CTG GCA GCT ATT ATG CAA AAC TGG ACC
 901  CTC TTC CCT TAT TTA AGC AGA GTG AGT TTC TGG AAC
 937  CAG TGG TGC CCC CCC CCC CGC CCC GGC CGC CGT CCT
 973  GCT CAA GGG AAG CCT CCC TGC AGA GCA GCA GAG CCC
1009  CTG GGC AGG AGC GCC GCG TCC CGC TCC CAG GAG ACA
1045  GCA TGC GCG GTC ACG CGG CAC TTC CTG TGC CTC CCA
1081  GCC CCA GTG CCC CGG AGT TCT TCA GGG CGA CAG GGA
1117  CCT CAG AAG ACT GGA TCC GAT CCA GAC AGA CGC CCA
1153  TTC TTG GTT CAG CTC AGT GTT TTC AAA AGG AAC GTG
1189  CTA CCG TGG GTA GAG CAC ACT GGT TCT CAG AAC ACG
1225  GCC GGC GCT TGA CGG TTG TCA CAG CTC CAG AAC AAA
1261  TCC TGG GAG ACA GGC GAG CGC GAG TCG CCG GGC AGG
1297  AAT TCC ACA CAC TCG TGC TGT TTT TGA TAC CTG CTT
1333  TTT GTT TTG TTT TGT AAA AAT GAT GCA CTT GAG AAA
1369  ATA AAA CGT CAG TGT TGA CAA AAA AAA AAA AAA AAA
```

Fig. 11

```
1   GAC TGC CGC AGC AGC AGC AAC AAC CGC TAG CCG AAG
    asp cys arg ser ser ser asn asn arg Xaa pro lys

37  GGT GGC GCG GCG CGG GCC GGC GGC CCG GCG CGG CCC
    gly gly ala ala arg ala gly gly pro ala arg pro

73  GTG AGC CTG CGG GAA GTC GTG CGC TAC CTC GGG GGT
    val ser leu arg glu val val arg tyr leu gly gly

109 AGC AGC GGC GCT GGC GGC CGC CTG ACC CGC GGC CGC
    ser ser gly ala gly gly arg leu thr arg gly arg

145 GTG CAG GGT CTG CTG GAA GAG GAG GCG GCG GCG CGG
    val gln gly leu leu glu glu glu ala ala ala arg

181 GGC CGC CTG GAG CGC ACC CGT CTC GGA GCG CTT GCG
    gly arg leu glu arg thr arg leu gly ala leu ala

217 CTG CCC CGC GGG GAC AGG CCC GGA CGG GCG CCA CCG
    leu pro arg gly asp arg pro gly arg ala pro pro

253 GCC GCC AGC GCC CGC GCG GCG CGG AAC AAG AGA GCT
    ala ala ser ala arg ala ala arg asn lys arg ala

289 GGC GAG GAG CGA GTG CTT GAA AAG GAG GAG GAG GAG
    gly glu glu arg val leu glu lys glu glu glu glu

325 GAG GAG GAG GAA GAC GAC GAG GAC GAC GAC GAC GAC
    glu glu glu glu asp asp glu asp asp asp asp asp

361 GTC GTG TCC GAG GGC TCG GAG GTG CCC GAG AGC GAT
    val val ser glu gly ser glu val pro glu ser asp

397 CGT CCC GCG GGT GCG CAG CAT CAC CAG CTG AAT GGC
    arg pro ala gly ala gln his his gln leu asn gly

433 GGC GAG CGC GGC CCG CAG ACC GCC AAG GAG CGG GCC
    gly glu arg gly pro gln thr ala lys glu arg ala

469 AAG GAG TGG TCG CTG TGT GGC CCC CAC CCT GGC CAG
    lys glu trp ser leu cys gly pro his pro gly gln
```

Fig. 11 (continued)

```
505  GAG GAA GGG CGG GGG CCG GCC GCG GGC AGT GGC ACC
     glu glu gly arg gly pro ala ala gly ser gly thr

541  CGC CAG GTG TTC TCC ATG GCG GCC TTG AGT AAG GAG
     arg gln val phe ser met ala ala leu ser lys glu

577  GGG GGA TCA GCC TCT TCG ACC ACC GGG CCT GAC TCC
     gly gly ser ala ser ser thr thr gly pro asp ser

613  CCG TCC CCG GTG CCT TTG CCC CCC GGG AAG CCA GCC
     pro ser pro val pro leu pro pro gly lys pro ala

649  CTC CCA GGA GCC GAT GGG ACC CCC TTT GGC TGC CCT
     leu pro gly ala asp gly thr pro phe gly cys pro

685  GCC GGG CGC AAA GAG AAG CCG GCA GAC CCC GTG GAG
     ala gly arg lys glu lys pro ala asp pro val glu

721  TGG ACA GTC ATG GAC GTC GTG GAG TAC TTC ACC GAG
     trp thr val met asp val val glu tyr phe thr glu

757  GCG GGC TTC CCT GAG CAA GCC ACG GCT TTC CAG GAG
     ala gly phe pro glu gln ala thr ala phe gln glu

793  CAG GAG ATC GAC GGC AAG TCC CTG CTG CTC ATG CAG
     gln glu ile asp gly lys ser leu leu leu met gln

829  CGC ACC GAT GTC CTC ACC GGC CTG TCC ATC CGC CTG
     arg thr asp val leu thr gly leu ser ile arg leu

865  GGG CCA GCG TTG AAA ATC TAT GAG CAC CAT ATC AAG
     gly pro ala leu lys ile tyr glu his his ile lys

901  GTG CTG CAG CAG GGT CAC TTC GAG GAC GAT GAC CCG
     val leu gln gln gly his phe glu asp asp asp pro

937  GAA GGC TTC CTG GGA TGA GCA CAG AGC CGC CGC GCC
     glu gly phe leu gly

973  CCT TGT CCC CAC CCC CAC CCC GCC TGG ACC CAT TCC
1009 TGC CTC CAT GTC ACC CAA GGT GTC CCA GAG GCC AGG
1045 AGC TGG ACT GGG CAG GCG AGG GGT GCG GAC CTA CCC
1081 TGA TTC TGG TAG GGG GCG GGG CCT TGC TGT GCT CAT
```

Fig. 11 (continued)

1117	TGC	TAC	CCC	CCC	ACC	CCG	TGT	GTG	TCT	CTG	CAC	CTG
1153	CCC	CCA	GCA	CAC	CCC	TCC	CGG	AGC	CTG	GAT	GTC	GCC
1189	TGG	GAC	TCT	GGC	CTG	CTC	ATT	TTG	CCC	CCA	GAT	CAG
1225	CCC	CCT	CCC	TCC	CTC	CTG	TCC	CAG	GAC	ATT	TTT	TAA
1261	AAG	AAA	AAA	AGG	AAA	AAA	AAA	AAT	TGG	GGA	GGG	GGC
1297	TGG	GAA	GGT	GCC	CCA	AGA	TCC	TCC	TCG	GCC	CAA	CCA
1333	GGT	GTT	TAT	TCC	TAT	ATA	TAT	ATA	TAT	ATG	TTT	TGT
1369	TCT	GCC	TGT	TTT	TCG	TTT	TTT	GGT	GCG	TGG	CCT	TTC
1405	TTC	CCT	CCC	ACC	ACC	ACT	CAT	GGC	CCC	AGC	CCT	GCT
1441	CGC	CCT	GTC	GGC	GGG	AGC	AGC	TGG	GAA	TGG	GAG	GAG
1477	GGT	GGG	ACC	TTG	GGT	CTG	TCT	CCC	ACC	CTC	TCT	CCC
1513	GTT	GGT	TCT	GTT	GTC	GCT	CCA	GCT	GGC	TGT	ATT	GCT
1549	TTT	TAA	TAT	TGC	ACC	GAA	GGG	TTG	TTT	TTT	TTT	TTT
1585	TAA	ATA	AAA	TTT	TAA	AAA	AAG	GAA	AAA	AAA	AAA	

Fig. 12

```
256      GCC AGC GCC CGC GCG GCG CGG AAC AAG AGA GCT
         ala ser ala arg ala ala arg asn lys arg ala

289  GGC GAG GAG CGA GTG CTT GAA AAG GAG GAG GAG GAG
     gly glu glu arg val leu glu lys glu glu glu glu

325  GAG GAG GAG GAA GAC GAC GAG GAC GAC GAC GAC GAC
     glu glu glu glu asp asp glu asp asp asp asp asp

361  GTC GTG TCC GAG GGC TCG GAG GTG CCC GAG AGC GAT
     val val ser glu gly ser glu val pro glu ser asp

397  CGT CCC GCG GGT GCG CAG CAT CAC CAG CTG AAT GGC
     arg pro ala gly ala gln his his gln leu asn gly

433  GGC GAG CGC GGC CCG CAG ACC GCC AAG GAG CGG GCC
     gly glu arg gly pro gln thr ala lys glu arg ala

469  AAG GAG TGG TCG CTG TGT GGC CCC CAC CCT GGC CAG
     lys glu trp ser leu cys gly pro his pro gly gln

505  GAG GAA GGG CGG GGG CCG GCC GCG GGC AGT GGC ACC
     glu glu gly arg gly pro ala ala gly ser gly thr

541  CGC CAG GTG TTC TCC ATG GCG GCC TTG AGT AAG GAG
     arg gln val phe ser met ala ala leu ser lys glu

577  GGG GGA TCA GCC TCT TCG ACC ACC GGG CCT GAC TCC
     gly gly ser ala ser ser thr thr gly pro asp ser

613  CCG TCC CCG GTG CCT TTG CCC CCC GGG AAG CCA GCC
     pro ser pro val pro leu pro pro gly lys pro ala

649  CTC CCA GGA GCC GAT GGG ACC CCC TTT GGC TGC CCT
     leu pro gly ala asp gly thr pro phe gly cys pro

685  GCC GGG CGC AAA GAG AAG CCG GCA GAC CCC GTG GAG
     ala gly arg lys glu lys pro ala asp pro val glu

721  TGG ACA GTC ATG GAC GTC GTG GAG TAC TTC ACC GAG
     trp thr val met asp val val glu tyr phe thr glu
```

Fig. 12 (continued)

```
 757  GCG GGC TTC CCT GAG CAA GCC ACG GCT TTC CAG GAG
      ala gly phe pro glu gln ala thr ala phe gln glu

 793  CAG GAG ATC GAC GGC AAG TCC CTG CTG CTC ATG CAG
      gln glu ile asp gly lys ser leu leu leu met gln

 829  CGC ACC GAT GTC CTC ACC GGC CTG TCC ATC CGC CTG
      arg thr asp val leu thr gly leu ser ile arg leu

 865  GGG CCA GCG TTG AAA ATC TAT GAG CAC CAT ATC AAG
      gly pro ala leu lys ile tyr glu his his ile lys

 901  GTG CTG CAG CAG GGT CAC TTC GAG GAC GAT GAC CCG
      val leu gln gln gly his phe glu asp asp asp pro

 937  GAA GGC TTC CTG GGA TGA GCA CAG AGC CGC CGC GCC
      glu gly phe leu gly

 973  CCT TGT CCC CAC CCC CAC CCC GCC TGG ACC CAT TCC
1009  TGC CTC CAT GTC ACC CAA GGT GTC CCA GAG GCC AGG
1045  AGC TGG ACT GGG CAG GCG AGG GGT GCG GAC CTA CCC
1081  TGA TTC TGG TAG GGG GCG GGG CCT TGC TGT GCT CAT
1117  TGC TAC CCC CCC ACC CCG TGT GTG TCT CTG CAC CTG
1153  CCC CCA GCA CAC CCC TCC CGG AGC CTG GAT GTC GCC
1189  TGG GAC TCT GGC CTG CTC ATT TTG CCC CCA GAT CAG
1225  CCC CCT CCC TCC CTC CTG TCC CAG GAC ATT TTT TAA
1261  AAG AAA AAA AGG AAA AAA AAA AAT TGG GGA GGG GGC
1297  TGG GAA GGT GCC CCA AGA TCC TCC TCG GCC CAA CCA
1333  GGT GTT TAT TCC TAT ATA TAT ATA TAT ATG TTT TGT
1369  TCT GCC TGT TTT TCG TTT TTT GGT GCG TGG CCT TTC
1405  TTC CCT CCC ACC ACC ACT CAT GGC CCC AGC CCT GCT
1441  CGC CCT GTC GGC GGG AGC AGC TGG GAA TGG GAG GAG
1477  GGT GGG ACC TTG GGT CTG TCT CCC ACC CTC TCT CCC
1513  GTT GGT TCT GTT GTC GCT CCA GCT GGC TGT ATT GCT
1549  TTT TAA TAT TGC ACC GAA GGG TTG TTT TTT TTT TTT
1585  TAA ATA AAA TTT TAA AAA AAG GAA AAA AAA AAA
```

Fig. 13

```
196                                 ACC CGT CTC GGA GCG CTT GCG
                                    thr arg leu gly ala leu ala

217  CTG CCC CGC GGG GAC AGG CCC GGA CGG GCG CCA CCG
     leu pro arg gly asp arg pro gly arg ala pro pro

253  GCC GCC AGC GCC CGC GCG GCG CGG AAC AAG AGA GCT
     ala ala ser ala arg ala ala arg asn lys arg ala

289  GGC GAG GAG CGA GTG CTT GAA AAG GAG GAG GAG GAG
     gly glu glu arg val leu glu lys glu glu glu glu

325  GAG GAG GAG GAA GAC GAC GAG GAC GAC GAC GAC GAC
     glu glu glu glu asp asp glu asp asp asp asp asp

361  GTC GTG TCC GAG GGC TCG GAG GTG CCC GAG AGC GAT
     val val ser glu gly ser glu val pro glu ser asp

397  CGT CCC GCG GGT GCG CAG CAT CAC CAG CTG AAT GGC
     arg pro ala gly ala gln his his gln leu asn gly

433  GGC GAG CGC GGC CCG CAG ACC GCC AAG GAG CGG GCC
     gly glu arg gly pro gln thr ala lys glu arg ala

469  AAG GAG TGG TCG CTG TGT GGC CCC CAC CCT GGC CAG
     lys glu trp ser leu cys gly pro his pro gly gln

505  GAG GAA GGG CGG GGG CCG GCC GCG GGC AGT GGC ACC
     glu glu gly arg gly pro ala ala gly ser gly thr

541  CGC CAG GTG TTC TCC ATG GCG GCC TTG AGT AAG GAG
     arg gln val phe ser met ala ala leu ser lys glu

577  GGG GGA TCA GCC TCT TCG ACC ACC GGG CCT GAC TCC
     gly gly ser ala ser ser thr thr gly pro asp ser

613  CCG TCC CCG GTG CCT TTG CCC CCC GGG AAG CCA GCC
     pro ser pro val pro leu pro pro gly lys pro ala

649  CTC CCA GGA GCC GAT GGG ACC CCC TTT GGC TGC CCT
     leu pro gly ala asp gly thr pro phe gly cys pro
```

Fig. 13 (continued)

685 GCC GGG CGC AAA GAG AAG CCG GCA GAC CCC GTG GAG
ala gly arg lys glu lys pro **ala** asp pro val glu

721 TGG ACA GTC ATG GAC GTC GTG GAG TAC TTC ACC GAG
trp thr val met asp val val glu tyr phe thr glu

757 GCG GGC TTC CCT GAG CAA GCC ACG GCT TTC CAG GAG
ala gly phe pro glu gln ala thr ala phe gln glu

793 CAG GAG ATC GAC GGC AAG TCC CTG CTG CTC ATG CAG
gln glu ile asp gly lys ser leu leu leu met gln

829 CGC ACC GAT GTC CTC ACC GGC CTG TCC ATC CGC CTG
arg thr asp val leu thr gly leu ser ile arg leu

865 GGG CCA GCG TTG AAA ATC TAT GAG CAC CAT ATC AAG
gly pro ala leu lys ile tyr glu his his ile lys

901 GTG CTG CAG CAG GGT CAC TTC GAG GAC GAT GAC CCG
val leu gln gln gly his phe glu asp asp asp pro

937 GAA GGC TTC CTG GGA TGA GCA CAG AGC CGC CGC GCC
glu gly phe leu gly

973 CCT TGT CCC CAC CCC CAC CCC GCC TGG ACC CAT TCC
1009 TGC CTC CAT GTC ACC CAA GGT GTC CCA GAG GCC AGG
1045 AGC TGG ACT GGG CAG GCG AGG GGT GCG GAC CTA CCC
1081 TGA TTC TGG TAG GGG GCG GGG CCT TGC TGT GCT CAT
1117 TGC TAC CCC CCC ACC CCG TGT GTG TCT CTG CAC CTG
1153 CCC CCA GCA CAC CCC TCC CGG AGC CTG GAT GTC GCC
1189 TGG GAC TCT GGC CTG CTC ATT TTG CCC CCA GAT CAG
1225 CCC CCT CCC TCC CTC CTG TCC CAG GAC ATT TTT TAA
1261 AAG AAA AAA AGG AAA AAA AAA AAT TGG GGA GGG GGC
1297 TGG GAA GGT GCC CCA AGA TCC TCC TCG GCC CAA CCA
1333 GGT GTT TAT TCC TAT ATA TAT ATA TAT ATG TTT TGT
1369 TCT GCC TGT TTT TCG TTT TTT GGT GCG TGG CCT TTC
1405 TTC CCT CCC ACC ACC ACT CAT GGC CCC AGC CCT GCT
1441 CGC CCT GTC GGC GGG AGC AGC TGG GAA TGG GAG GAG
1477 GGT GGG ACC TTG GGT CTG TCT CCC ACC CTC TCT CCC
1513 GTT GGT TCT GTT GTC GCT CCA GCT GGC TGT ATT GCT
1549 TTT TAA TAT TGC ACC GAA GGG TTG TTT TTT TTT TTT
1585 TAA ATA AAA TTT TAA AAA AAG GAA AAA AAA AAA

Fig. 14

```
  1  GTG GAA AAT AGC AAC TGT GTT TCT CAA GGA TCC AAT
 37  CCC AAC CTA AGG TGG CAG CGC ACA ATG AAG AAT CAA
                                     met lys asn gln

 73  GAC AAA AAG AAC GGG GCT GCC AAA CAG CCC AAC CCC
     asp lys lys asn gly ala ala lys gln pro asn pro

109  AAA AGC AGC CCG GGA CAG CCG GAA GCA GGA GCG GAG
     lys ser ser pro gly gln pro glu ala gly ala glu

145  GGA GCC CAG GGG CGG CCC GGC CGG CCG GCC CCC GCC
     gly ala gln gly arg pro gly arg pro ala pro ala

181  CGA GAA GCC GAA GGT GCC AGC AGC CAG GCT CCC GGG
     arg glu ala glu gly ala ser ser gln ala pro gly

217  AGG CCG GAG GGG GCT CAA GCC AAA ACT GCT CAG CCT
     arg pro glu gly ala gln ala lys thr ala gln pro

253  GGG GCG CTC TGT GAT GTC TCT GAG GAG CTG AGC CGC
     gly ala leu cys asp val ser glu glu leu ser arg

289  CAG TTG GAA GAC ATA CTC AGT ACA TAC TGT GTG GAC
     gln leu glu asp ile leu ser thr tyr cys val asp

325  AAC AAC CAG GGG GCC CCG GGT GAG GAT GGG GTC CAG
     asn asn gln gly ala pro gly glu asp gly val gln

361  GGT GAG CCC CCT GAA CCT GAA GAT GCA GAG AAG TCT
     gly glu pro pro glu pro glu asp ala glu lys ser

397  CGC GCC TAT GTG GCA AGG AAT GGG GAG CCG GAG CCG
     arg ala tyr val ala arg asn gly glu pro glu pro

433  GGC ACC CCA GTA GTC AAT GGC GAG AAG GAG ACC TCC
     gly thr pro val val asn gly glu lys glu thr ser

469  AAG GCA GAG CCG GGC ACG GAA GAG ATC CGG ACG AGC
     lys ala glu pro gly thr glu glu ile arg thr ser

505  GAT GAG GTC GGA GAC CGA GAC CAC CGG AGG CCA CAG
     asp glu val gly asp arg asp his arg arg pro gln
```

Fig. 14 (continued)

```
541  GAA AAG AAG AAG GCC AAG GGT CTG GGA AAG GAG ATC
     glu lys lys lys ala lys gly leu gly lys glu ile

577  ACG CTG CTG ATG CAG ACA CTG AAC ACG CTG AGC ACC
     thr leu leu met gln thr leu asn thr leu ser thr

613  CCA GAG GAG AAG CTG GCG GCT CTG TGC AAG AAG TAT
     pro glu glu lys leu ala ala leu cys lys lys tyr

649  GCG GAA CTG CTC GAG GAG CAC CGG AAC TCG CAG AAG
     ala glu leu leu glu glu his arg asn ser gln lys

685  CAG ATG AAG CTG CTG CAG AAG AAG CAG AGC CAG CTG
     gln met lys leu leu gln lys lys gln ser gln leu

721  GTG CAG GAG AAG GAC CAC CTG CGT GGC GAG CAC AGC
     val gln glu lys asp his leu arg gly glu his ser

757  AAG GCC ATC CTG GCC CGC AGC AAG CTC GAG AGC CTG
     lys ala ile leu ala arg ser lys leu glu ser leu

793  TGC CGG GAG CTG CAG CGG CAC AAC CGC TCG CTC AAG
     cys arg glu leu gln arg his asn arg ser leu lys

829  GAA GAA GGT GTG CAG CGA GCC CGA GAG GAG GAG GAG
     glu glu gly val gln arg ala arg glu glu glu glu

865  AAG CGC AAG GAG GTG ACG TCA CAC TTC CAG ATG ACG
     lys arg lys glu val thr ser his phe gln met thr

901  CTC AAC GAC ATT CAG CTG CAG ATG GAG CAG CAC AAC
     leu asn asp ile gln leu gln met glu gln his asn

937  GAG CGC AAC TCC AAG CTG CGC CAG GAG AAC ATG GAG
     glu arg asn ser lys leu arg gln glu asn met glu

973  CTG GCC GAG CGG CTC AAG AAG CTG ATT GAG CAG TAC
     leu ala glu arg leu lys lys leu ile glu gln tyr

1009 GAG CTG CGA GAA GAG CAC ATC GAC AAA GTC TTC AAA
     glu leu arg glu glu his ile asp lys val phe lys
```

Fig. 14 (continued)

1045 CAC AAG GAT CTG CAG CAG CAG CTG GTG GAC GCC AAG
his lys asp leu gln gln gln leu val asp ala lys

1081 CTC CAG CAG GCC CAG GAG ATG CTG AAG GAG GCA GAG
leu gln gln ala gln glu met leu lys glu ala glu

1117 GAG CGG CAC CAG CGG GAG AAG GAC TTT CTC CTG AAG
glu arg his gln arg glu lys asp phe leu leu lys

1153 GAG GCC GTG GAG TCC CAG AGG ATG TGC GAG CTG ATG
glu ala val glu ser gln arg met cys glu leu met

1189 AAG CAA CAG GAG ACC CAC CTG AAG CAG CAG CTT GCC
lys gln gln glu thr his leu lys gln gln leu ala

1225 CTA TAC ACA GAG AAG TTT GAG GAG TTC CAG AAC ACT
leu tyr thr glu lys phe glu glu phe gln asn thr

1261 CTT TCC AAA AGC AGC GAG GTG TTC ACC ACA TTC AAA
leu ser lys ser ser glu val phe thr thr phe lys

1297 CAG GAA ATG GAA AAG ATG ACA AAG AAG ATC AAG AAG
gln glu met glu lys met thr lys lys ile lys lys

1333 CTG GAG AAA GAG ACC ACC ATG TAC CGT TCC CGG TGG
leu glu lys glu thr thr met tyr arg ser arg trp

1369 GAG AGC AGC AAC AAG GCC CTG CTT GAG ATG GCT GAG
glu ser ser asn lys ala leu leu glu met ala glu

1405 GAG AAA ACA CTC CGG GAC AAA GAG CTG GAA GGC CTG
glu lys thr **leu** arg asp lys glu leu glu gly leu

1441 CAG GTG AAA ATC CAG CGG CTG GAG AAG CTG TGC CGG
gln val lys ile gln arg leu glu lys leu cys arg

1477 GCA CTG CAG ACA GAG CGC AAT GAC CTG AAC AAG AGG
ala leu gln thr glu arg asn asp leu asn lys arg

1513 GTG CAG GAC CTG AGT GCC GGT GGC CAG GGC CCC GTC
val gln asp leu ser ala gly gly gln gly **pro val**

Fig. 14 (continued)

1549 TCC GAC AGC GGT CCT GAG CGG AGG CCA GAG CCC GCC
ser asp ser gly pro glu arg arg pro **glu pro ala**

1585 ACC ACC TCC AAG GAG CAG GGT GTC GAG GGC CCC GGG
thr thr ser lys glu gln gly val glu gly pro gly

1621 GCT CAA GTA CCC AAC TCT CCA AGG GCC ACA GAC GCT
ala gln **val** pro **asn** ser pro arg **ala** thr **asp** ala

1657 TCC TGC TGC GCA GGT GCA CCC AGC ACA GAG GCA TCA
ser cys **cys ala** gly ala pro ser thr glu ala ser

1693 GGC CAG ACA GGG CCC CAG GAG CCC ACC ACT GCC ACT
gly gln thr gly pro gln glu pro thr **thr** ala **thr**

1729 GCC TAG AGA GCT TGG TGC TGG GGT GTG CCA GGA AGG
ala

1765 GAG CAG GCA GCC CAG CCA GGC CTG GCC CAG CCC AGG
1801 CTC CCA TGC TAA GCA GTC CGG TGC TGA GGC CAG GAT
1837 GTT CTG ACC TGG CTG GCA CCT GAC CCT CTG CAG TCT
1873 TGG ATT TTG TGG GTC AGT TTT ACA TGC ATA TGG CAC
1909 ACA TGC AAG GCC TCA CAC ATT TGT GTC TCT AAG TGT
1945 ACT GTG GGC TTG CAT CGG GGG TGA CGA TGG ACA GAT
1981 GAA GCC AGC GGC TCC CTT GTG AGC TGA AGT CTT ACG
2017 GAG GAG ACG GCG TCT GCA CTG CCA TCG CAG TGA CCT
2053 GCA GGA CGA GTT CCT TGA GCT TTC CCT GCC TGC TTT
2089 GAG GCT GAG ACC CCT CCC GGC CCT TCA GAG CTC CTG
2125 ACA GGT GAT ACA CAC CCA GCC TTG ACC GCA CTT CTC
2161 TTG GGT AGC TGG GCT CTC CTA GCC TCC CCC AGA GGC
2197 GCC ATT GCT TCT CTT GAC TTG GAG AGG GGA TGC CCA
2233 GGC GTG GCC TTG GCA GGC ACT GGG AGC TAG TGA TTG
2269 GGC TGC TCT CCT GCC TCG AGC AGG GGC AGG AGT GTT
2305 TCT GGT GGG ATG ATG CGC TCG CTG GTC AGG AGC CCC
2341 GTG GGC GCT GCT TCC CCC GCC CTC TGG TGA TGC CAG
2377 GAC CAG GCC AGT GAT GCT TCT CAG TAG CCT TAC CAT
2413 TCA CAG GTG CCT CTC CAG CCC GCA CAG TGA GTG ACA
2449 AGA TCA TCC AAA GGA TTC CTT CTG AAG GTG TTC GTT
2485 TCG TTT TGT TTT GTT GCA CGT GAC GGT TTG TAT TGA
2521 GGA CCC TCT GAG GAA GAG GGG TGC TGT AGC AGT GGT
2557 CCC TGC GTG CCT GGC TCC AGT GTC CTG CCC TCC CCC
2593 CCC TCG CCA TGG CTC CTC GGC CGC CTT GGT GCT GAG
2629 GTT TCT GTT TGG TGA GAT CAG GTT GTC TGT TCA GAG

Fig. 14 (continued)

```
2665  AGA AGA GGC GTC TGA TGG CTT TGC CGC CAG CTT GCC
2701  TGC GGG CCT CAA TCC CGG GAG GCC GCC CGG TTC CCG
2737  TCA CTG TTG TCC CCG TGC AGT GCG TTG CTG GTC CCC
2773  AGG ACC AGC TGC TCG TTT GCT GTA TGG GTC AGT TTC
2809  TGC TTC CTG CCC CCC ACT CCA CCT AAC TGC AAT CCT
2845  TGG GGT TTC CCT GGT TCT CGT CCC TGG TAC CTC TGT
2881  GCC CAA GAA GTA GCC TTC TTT GGG ATT CTT GTT CTG
2917  CCC ATG CGG GAG CTG CTG CTG TCT GAC AGG TGA GGC
2953  CTG AGA CTC AGC GGC TGA CAG AGC TGC AGA GCT CTG
2989  CAC GGT GGC TCC CGG GGC GGC CTC TGT GTG CTG CAC
3025  ACC GCT GCT CTG CTG GCA CTG GCC AGT CTG TGC AGA
3061  GCA TTT GAG TAC TGG CTC AGG AGG GAG GGC TCT GCT
3097  GGC CTC GAG GGA CAG CGC CAC GTC TCC AGC TGG GCT
3133  CAG GGA GAG CCC CAG ACT GGC TGC GTA GGG TGC TTG
3169  GGG TTT GCT TCT TGC AGT ATT TCT TGG AAG CTG TTT
3205  TGT TGT CCT GCT ATT CCT TCA TCT TCC ACA GTC CAC
3241  GCT CAG CCT TTA ACT TGG ATC CCT CAC ATA ACA GGG
3277  TTC ATG AGA CCC GCA AGT ACG CCC AAG CTA CGT ATG
3313  GCT GAG GCC AGC TGG CAG GTG AAT GGC ACG CCA TTG
3349  CTG CTG CTA ATC CCT GGC ATA TCT TTA GTT CAC CTC
3385  GAA ATG CCC CCG CCA CAG TGC AAG CAG TGA GTC CAC
3421  GTG CCA CCC TGG GCT GAA TCC CAC CCC CTG TGA GTG
3457  TTG CCC GAG ATT GTG TCT CTT CTG AAT GCC TTC ACT
3493  GGG AAT GGC CTC TGC CGC CTC CTG CTC AGG GAG GCT
3529  TTC CCC TTC CCT CAG CCC CTG TGC CAG ACT GAG GTA
3565  CAA GAA CCG CCA AGC CCA TGC AAG GTG TGG CTA GGC
3601  GCC AGG GTG CAG GAA GGA GGC AGG TAG CTG CCT GCA
3637  CCC TTG AAA GCC AAG AGG CCT ACG GTG GCC TCC ATC
3673  CTG GCT TGC CTC ACT TCA GCT ACC TCG CAT AGC CCA
3709  GGG GTG GGG CTA TTG GAT TCC AGG GTG GGG GGA TGG
3745  GAA GCT GCA GGG GGC AGG TGG CTC TCA CTA GGC TTC
3781  CCA GCT CAG GAA TGT GGG CCT CAG GTA GGG GAG AGC
3817  CTT TGC TCC ACT CCA CCC ATT TGC AGG CAT CTA GGC
3853  CAG TCT AGA TGG CGA CCC CTT CTC TTC CTC TCC ATT
3889  GAC CAA ATC GTA CCT GTC TCT CCA GCT GCT CGC TTG
3925  CTC TGC TTT CCA AAG TCA GCC CAG GTA CCC AGG TGC
3961  CGC CCA CAT TGG CCT GGA ACC TGG ACC AGA GGC AAG
3997  GGA GGT GGC CTA TCC TTG AGT GAT AGC CAG TGC CTT
4033  CCT CAC CCG GTG GCT TCC ATG CCT GTG ACC TCA GAT
4069  TTA GGA CCA AGA GCT GTG TTG GTT TCT TAC GTT GTG
4105  AGC TTT CCC TCC AGG GGA CCA CAG CAG GTG AGG CTC
4141  GGA GCC CAG AGC CCT TGG CGC CGC CAG CAG TAA CTT
4177  GTG TCC GGA CCT TGT CCA GCT GAG CGC TTC GTG TAT
```

Fig. 14 (continued)

4213 GAC TCA GCT TCG TGT GTG AGT CCA GCG GAG TGC GTC
4249 ACG TGA CCT AGA CTC AGC GGT GTC AGC CGC ACT TTG
4285 ATT TGT TTG TTT TCC ATG AGG TTT TTG GAC CAT GGG
4321 CTT AGC TCA GGC AAC TTT TCT GTA AGG AGA ATG TTA
4357 ACT TTC TGT AAA GAT GCT TAT TTA ACT AAC GCC TGC
4393 TTC CCC CAC TCC CAA CCA GGT GGC CAC CGA GAG CTC
4429 ACC AGG AGG CCA ATA GAG CTG CTC CAG CTC TCC CAT
4465 CTT GCA CCG CAC AAA GGT GGC CGC CCC AGG GAC AGC
4501 CAG GCA CCT GCC TGG GGG AGG GGC TTC TCT TCC TTA
4537 TGG CCT GGC CAT CTA GAT TGT TTA AAG TTG TGC TGA
4573 CAG CTT TTT TTG GTT TTT TGG TTT TTG TTT TTG TTT
4609 TTG TTT TTG TTT TTG TCT ACT TTT GGT ATT CAC AAC
4645 AGC CAG GGA CTT GAT TTT GAT GTA TTT TAA GCC ACA
4681 TTA AAT AAA GAG TCT GTT GCC TTA AAA AAA AAA AAA
4717 AAA AAA

Fig. 15

```
  1  GAC GCC TCA GAG CGG AAC AGG GAA GTG AAT CAG GCG
 37  CCG GGT AGT GGG TTG CTG GGC TGG GCT TGC TGA GGT
 73  AGA GGC AGC GCC AAG AAG AGG CCT TTG CCG CTG GTC
109  GGG ATT GGG ATG TCG AAG AAC ACA GTG TCG TCG GCC
                 met ser lys asn thr val ser ser ala

145  CGC TTC CGG AAG GTG GAC GTG GAT GAA TAT GAC GAG
     arg phe arg lys val asp val asp glu tyr asp glu

181  AAC AAG TTC GTG GAC GAA GAA GAT GGG GGC GAC GGC
     asn lys phe val asp glu glu asp gly gly asp gly

217  CAG GCC GGG CCC GAC GAG GGC GAG GTG GAC TCC TGC
     gln ala gly pro asp glu gly glu val asp ser cys

253  CTG CGG CAA GGA AAC ATG ACA GCT GCC CTA CAG GCA
     leu arg gln gly asn met thr ala ala leu gln ala

289  GCT CTG AAG AAC CCC CCT ATC AAC ACC AAG AGT CAG
     ala leu lys asn pro pro ile asn thr lys ser gln

325  GCA GTG AAG GAC CGG GCA GGC AGC ATT GTC TTG AAG
     ala val lys asp arg ala gly ser ile val leu lys

361  GTG CTC ATC TCT TTT AAA GCT AAT GAT ATA GAA AAG
     val leu ile ser phe lys ala asn asp ile glu lys

397  GCA GTT CAA TCT CTG GAC AAG AAT GGT GTG GAT CTC
     ala val gln ser leu asp lys asn gly val asp leu

433  CTA ATG AAG TAT ATT TAT AAA GGA TTT GAG AGC CCG
     leu met lys tyr ile tyr lys gly phe glu ser pro

469  TCT GAC AAT AGC AGT GCT ATG TTA CTG CAA TGG CAT
     ser asp asn ser ser ala met leu leu gln trp his

505  GAA AAG GCA CTT GCT GCT GGA GGA GTA GGG TCC ATT
     glu lys ala leu ala ala gly gly val gly ser ile

541  GTT CGT GTC TTG ACT GCA AGA AAA ACT GTG TAG TCT
     val arg val leu thr ala arg lys thr val
```

Fig. 15 (continued)

```
 577  GGC AGG AAG TGG ATT ATC TGC CTC GGG AGT GGG AAT
 613  TGC TGG TAC AAA GAC CAA AAC AAC CAA ATG CCA CCG
 649  CTG CCC TGT GGG TAG CAT CTG TTT CTC TCA GCT TTG
 685  CCT TCT TGC TTT TTC ATA TCT GTA AAG AAA AAA ATT
 721  ACA TAT CAG TTG TCC CTT TAA TGA AAA TTG GGA TAA
 757  TAT AGA AGA AAT TGT GTT AAA ATA GAA GTG TTT CAT
 793  CCT TTC AAA ACC ATT TCA GTG ATG TTT ATA CCA ATC
 829  TGT ATA TAG TAT AAT TTA CAT TCA AGT TTT AAT TGT
 865  GCA ACT TTT AAC CCT GTT GGC TGG TTT TTG GTT CTG
 901  TTT GGT TTT GTA TTA TTT TTA ACT AAT ACT GAA AAA
 937  TTT GGT CAG AAT TTG AGG CCA GTT TCC TAG CTC ATT
 973  GCT AGT CAG GAA ATG ATA TTT ATA AAA AAT ATG AGA
1009  GAC TGG CAG CTA TTA ACA TTG CAA AAC TGG ACC ATA
1045  TTT CCC TTA TTT AAT AAG CAA AAT ATG TTT TTG GAA
1081  TAA GTG GTG GGT GAA TAC CAC TGC TAA GTT ATA GCT
1117  TTG TTT TTG CTT GCC TCC TCA TTA TCT GTA CTG TGG
1153  GTT TAA GTA TGC TAC TTT CTC TCA GCA TCC AAT AAT
1189  CAT GGC CCC TCA ATT TAT TTG TGG TCA CGC AGG GTT
1225  CAG AGC AAG AAG TCT TGC TTT ATA CAA ATG TAT CCA
1261  TAA AAT ATC AGA GCT TGT TGG GCA TGA ACA TCA AAC
1297  TTT TGT TCC ACT AAT ATG GCT CTG TTT GGA AAA AAC
1333  TGC AAA TCA GAA AGA ATG ATT TGC AGA AAG AAA GAA
1369  AAA CTA TGG TGT AAT TTA AAC TCT GGG CAG CCT CTG
1405  AAT GAA ATG CTA CTT TCT TTA GAA ATA TAA TAG CTG
1441  CCT TAG ACA TTA TGA GGT ATA CAA CTA GTA TTT AAG
1477  ATA CCA TTT AAT ATG CCC CGT AAA TGT CTT CAG TGT
1513  TCT TCA GGG TAG TTG GGA TCT CAA AAG ATT TGG TTC
1549  AGA TCC AAA CAA ATA CAC ATT CTG TGT TTT AGC TCA
1585  GTG TTT TCT AAA AAA AGA AAC TGC CAC ACA GCA AAA
1621  AAT TGT TTA CTT TGT TGG ACA AAC CAA ATC AGT TCT
1657  CAA AAA ATG ACC GGT GCT TAT AAA AAG TTA TAA ATA
1693  TCG AGT AGC TCT AAA ACA AAC CAC CTG ACC AAG AGG
1729  GAA GTG AGC TTG TGC TTA GTA TTT ACA TTG GAT GCC
1765  AGT TTT GTA ATC ACT GAC TTA TGT GCA AAC TGG TGC
1801  AGA AAT TCT ATA AAC TCT TTG CTG TTT TTG ATA CCT
1837  GCT TTT TGT TTC ATT TTG TTT TGT TTT GTA AAA ATG
1873  ATA AAA CTT CAG AAA ATA AAA TGT CAG TGT TGA ATA
1909  ATT AAA AAA AAA AAA AA
```

Fig. 16

```
  1  GAA GAG CGA GTA CTT GAG AAA GAA GAG GAA GAA GAT
     glu glu arg val leu glu lys glu glu glu glu asp

 37  GAT GAT GAA GAT GAA GAT GAA GAA GAT GAT GTG TCA
     asp asp glu asp glu asp glu glu asp asp val ser

 73  GAG GGC TCT GAA GTG CCC GAG AGT GAC CGT CCT GCA
     glu gly ser glu val pro glu ser asp arg pro ala

109  GGT GCC CAG CAC CAC CAG CTT AAC GGC GAG CGG GGA
     gly ala gln his his gln leu asn gly glu arg gly

145  CCT CAG AGT GCC AAG GAG AGG GTC AAG GAG TGG ACC
     pro gln ser ala lys glu arg val lys glu trp thr

181  CCC TGC GGA CCG CAC CAG GGC CAG GAT GAA GGG CGG
     pro cys gly pro his gln gly gln asp glu gly arg

217  GGG CCA GCC CCG GGC AGC GGC ACC CGC CAG GTG TTC
     gly pro ala pro gly ser gly thr arg gln val phe

253  TCC ATG GCA GCC ATG AAC AAG GAA GGG GGA ACA GCT
     ser met ala ala met asn lys glu gly gly thr ala

289  TCT GTT GCC ACC GGG CCA GAC TCC CCG TCC CCC GTG
     ser val ala thr gly pro asp ser pro ser pro val

325  CCT TTG CCC CCA GGC AAA CCA GCC CTA CCT GGG GCC
     pro leu pro pro gly lys pro ala leu pro gly ala

361  GAC GGG ACC CCC TTT GGC TGT CCT CCC GGG CGC AAA
     asp gly thr pro phe gly cys pro pro gly arg lys

397  GAG AAG CCA TCT GAT CCC GTC GAG TGG ACC GTG ATG
     glu lys pro ser asp pro val glu trp thr val met

433  GAT GTC GTC GAA TAT TTT ACT GAG GCT GGA TTC CCG
     asp val val glu tyr phe thr glu ala gly phe pro

469  GAG CAG GCG ACA GCT TTC CAA GAG CAG GAA ATT GAT
     glu gln ala thr ala phe gln glu gln glu ile asp
```

Fig. 16 (continued)

```
505  GGC AAA TCT TTG CTG CTC ATG CAG CGC ACA GAT GTG
     gly lys ser leu leu leu met gln arg thr asp val

541  CTC ACC GGC CTG TCC ATC CGC CTC GGG CCA GCC CTG
     leu thr gly leu ser ile arg leu gly pro ala leu

577  AAA ATC TAC GAG CAC CAC ATC AAG GTG CTT CAG CAA
     lys ile tyr glu his his ile lys val leu gln gln

613  GGC CAC TTT GAG GAT GAT GAC CCC GAT GGC TTC TTA
     gly his phe glu asp asp asp pro asp gly phe leu

649  GGC TGA GCG CCC AGC CTC ACC CCT GCC CCA GCC CAT
     gly

685  TCC GGC CCC CAT CTC ACC CAA GAT CCC CCA GAG TCC
721  AGG AGC TGG ACG GGG ACA CCC TCA GCC CTC ATA ACA
757  GAT TCC AAG GAG AGG GCA CCC TCT TGT CCT TAT CTT
793  TGC CCC TTG TNT CTG TCT CAC ACA CAT CTG CTC CTC
829  AGC ACG TCG GTG TGG GGA GGG GAT TGC TCC TTA AAC
865  CCC AGG TGG CTG ACC CTC CCC ACC CAG TCC AGG ACA
901  TTT TAG GAA AAA AAA AAT GAA ATG TGG GGG GCT TCT
937  CAT CTC CCC AAG ATC CTC TTC CGT TCA GCC AGA TGT
973  TTC CTG TAT AAA TGT TTG GAT CTG CCT GTT TAT TTT
1009 GGT GGG TGG TCT TTC CTC CCT CCC CTA CCA CCC ATG
1045 CCC CCC TTC TCA GTC TGC CCC TGG CCT CCA GCC CCT
1081 AGG GGA CTA GCT GGG TTG GGG TTC CTC GGG CCT TTT
1117 CTC TCC TCC CTC TTT TCT TTC TGT TGA TTG TCG CTC
1153 CAG CTG GCT GTA TTG CTT TTT AAT ATT GCA CCG AAG
1189 GTT TTT TAA ATA AAA TTT TA
```

Fig. 17

```
1    CA AAA AGC AGC CCA GGA CAA CCG GAA GCA GGA CCC GAG GGA GCC
        lys ser ser pro gly gln pro glu ala gly pro glu gly ala

45   CAG GAG CGG CCC AGC CAG GCG GCT CCT GCA GTA GAA GCA GAA GGT
     gln glu arg pro ser gln ala ala pro ala val glu ala glu gly

90   CCC GGC AGC AGC CAG GCT CCT CGG AAG CCG GAG GGG GCT CAA GCC
     pro gly ser ser gln ala pro arg lys pro glu gly ala gln ala

135  AGA ACG GCT CAG TCT GGG GCC CTT CGT GAT GTC TCT GAG GAG CTG
     arg thr ala gln ser gly ala leu arg asp val ser glu glu leu

180  AGC CGC CAA CTG GAA GAC ATA CTG AGC ACA TAC TGT GTG GAC AAT
     ser arg gln leu glu asp ile leu ser thr tyr cys val asp asn

225  AAC CAG GGG GGC CCC GGC GAG GAT GGG GCA CAG GGT GAG CCG GCT
     asn gln gly gly pro gly glu asp gly ala gln gly glu pro ala

270  GAA CCC GAA GAT GCA GAG AAG TCC CGG ACC TAT GTG GCA AGG AAT
     glu pro glu asp ala glu lys ser arg thr tyr val ala arg asn

315  GGG GAG CCT GAA CCA ACT CCA GTA GTC TAT GGA GAG AAG GAA CCC
     gly glu pro glu pro thr pro val val tyr gly glu lys glu pro

360  TCC AAG GGG GAT CCA AAC ACA GAA GAG ATC CGG CAG AGT GAC GAG
     ser lys gly asp pro asn thr glu glu ile arg gln ser asp glu

405  GTC GGA GAC CGA GAC CAT CGA AGG CCA CAG GAG AAG AAA AAA GCC
     val gly asp arg asp his arg arg pro gln glu lys lys lys ala

450  AAG GGT TTG GGG AAG GAG ATC ACG TTG CTG ATG CAG ACA TTG AAT
     lys gly leu gly lys glu ile thr leu leu met gln thr leu asn

495  ACT CTG AGT ACC CCA GAG GAG AAG CTG GCT GCT CTG TGC AAG AAG
     thr leu ser thr pro glu glu lys leu ala ala leu cys lys lys

540  TAT GCT GAA CTG CTG GAG GAG CAC CGG AAT TCA CAG AAG CAG ATG
     tyr ala glu leu leu glu glu his arg asn ser gln lys gln met

585  AAG CTC CTA CAG AAA AAG CAG AGC CAG CTG GTG CAA GAG AAG GAC
     lys leu leu gln lys lys gln ser gln leu val gln glu lys asp

630  CAC CTG CGC GGT GAG CAC AGC AAG GCC GTC CTG GCC CGC AGC AAG
     his leu arg gly glu his ser lys ala val leu ala arg ser lys

675  CTT GAG AGC CTA TGC CGT GAG CTG CAG CGG CAC AAC CGC TCC CTC
     leu glu ser leu cys arg glu leu gln arg his asn arg ser leu
```

Fig. 17 (continued)

720 AAG GAA GAA GGT GTG CAG CGG GCC CGG GAG GAG GAG GAG AAG CGC
lys glu glu gly val gln arg ala arg glu glu glu glu lys arg

765 AAG GAG GTG ACC TCG CAC TTC CAG GTG ACA CTG AAT GAC ATT CAG
lys glu val thr ser his phe gln **val** thr leu asn asp ile gln

810 CTG CAG ATG GAA CAG CAC AAT GAG CGC AAC TCC AAG CTG CGC CAA
leu gln met glu gln his asn glu arg asn ser lys leu arg gln

855 GAG AAC ATG GAG CTG GCT GAG AGG CTC AAG AAG CTG ATT GAG CAG
glu asn met glu leu ala glu arg leu lys lys leu ile glu gln

900 TAT GAG CTG CGC GAG GAG CAT ATC GAC AAA GTC TTC AAA CAC AAG
tyr glu leu arg glu glu his ile asp lys val phe lys his lys

945 GAC CTA CAA CAG CAG CTG GTG GAT GCC AAG CTC CAG CAG GCC CAG
asp leu gln gln gln leu val asp ala lys leu gln gln ala gln

990 GAG ATG CTA AAG GAG GCA GAA GAG CGG CAC CAG CGG GAG AAG GAT
glu met leu lys glu ala glu glu arg his gln arg glu lys asp

1035 TTT CTC CTG AAA GAG GCA GTA GAG TCC CAG AGG ATG TGT GAG CTG
phe leu leu lys glu ala val glu ser gln arg met cys glu leu

1080 ATG AAG CAG CAA GAG ACC CAC CTG AAG CAA CAG CTT GCC CTA TAC
met lys gln gln glu thr his leu lys gln gln leu ala leu tyr

1125 ACA GAG AAG TTT GAG GAG TTC CAG AAC ACA CTT TCC AAA AGC AGC
thr glu lys phe glu glu phe gln asn thr leu ser lys ser ser

1170 GAG GTA TTC ACC ACA TTC AAG CAG GAG ATG GAA AAG ATG ACT AAG
glu val phe thr thr phe lys gln glu met glu lys met thr lys

1215 AAG ATC AAG AAG CTG GAG AAA GAA ACC ACC ATG TAC CGG TCC CGG
lys ile lys lys leu glu lys glu thr thr met tyr arg ser arg

1260 TGG GAG AGC AGC AAC AAG GCC CTG CTT GAG ATG GCT GAG GAG AAA
trp glu ser ser asn lys ala leu leu glu met ala glu glu lys

1305 ACA GTC CGG GAT AAA GAA CTG GAG GGC CTG CAG GTA AAA ATC CAA
thr **val** arg asp lys glu leu glu gly leu gln val lys ile gln

1350 CGG CTG GAG AAG CTG TGC CGG GCA CTG CAG ACA GAG CGC AAT GAC
arg leu glu lys leu cys arg ala leu gln thr glu arg asn asp

1395 CTG AAC AAG AGG GTA CAG GAC CTG AGT GCT GGT GGC CAG GGC TCC
leu asn lys arg val gln asp leu ser ala gly gly gln gly **ser**

1440 CTC ACT GAC AGT GGC CCT GAG AGG AGG CCA GAG GGG CCT GGG GCT
leu thr asp ser gly pro glu arg arg pro glu gly pro gly ala

Fig. 17 (continued)

1485 CAA GCA CCC AGC TCC CCC AGG GTC ACA GAA GCG CCT TGC TAC CCA
gln **ala** pro **ser** ser pro arg **val** thr **glu** ala **pro** cys **tyr** **pro**

1530 GGA GCA CCG AGC ACA GAA GCA TCA GGC CAG ACT GGG CCT CAA GAG
gly ala pro ser thr glu ala ser gly gln thr gly pro gln glu

1575 CCC ACC TCC GCC AGG GCC TAG AGA GCC TGG TGT TGG GTC ATG CTG
pro thr **ser** ala **arg** ala ***

1620 GGA AGG GAG CGG CAG CCC AGC CAG GCC TGG CCC ATA AAA GGC TCC
1665 CAT GCT GAG CAG CCC ATT GCT GAA GCC AGG ATG TTC TTG ACC TGG
1710 CTG GCA TCT GGC ACT TGC AAT TTT GGA TTT TGT GGG TCA GTT TTA
1755 CGT ACA TAG GGC ATT TTG CAA GGC CTT GCA AAT GCA TTT ATA CCT
1800 GTA AGT GTA CAG TGG GCT TGC ATT GGG GAT GGG GGT GTG TAC AGA
1845 TGA AGT CAG TGG CTT GTC TGT GAG CTG AAG AGT CTT GAG AGG GGC
1890 TGT CAT CTG TAG CTG CCA TCA CAG TGA GTT GGC AGA AGT GAC TTG
1935 AGC ATT TCT CTG TCT GAT TTG AGG CTC AGA CCC CTC CCT GCC CTT
1980 TCA GAG CTC AAA ACA AGT AAT ACA CCA AGG TCT TGA CTG CAT TTG
2025 TCT TGT GAG CAG GGC TTG CTT GGT CAG CTC AGG CCC TCC TAG CTG
2070 CTT GGA GGC TCC TTT GAT TCT CTA GAC CTG GAA AAG GTG TCC CTA
2115 GGC AGA GCC CTG GCA GGG CGC TCA GAG CTG GGA TTT CCT GCC TGG
2160 AAC AAG GGA CCT GGA GAA TGT TTT TGC GTG GGA TGA TGT GCT GGT
2205 CAG GAG CCC CTT GGG CAT CGC TTC CCC TGC CCT TTG GTA GTG CCA
2250 GGA CCA GGC CAA TGA TGC TTC TCA GTA GCC TTA TCA TTC ACA GGT
2295 GCC TCT CTA GCC TGC ACA AAT GAT TGA CAA GAG ATC ACC CAA AGG
2340 ATT ATT TCT GAA GGT GTT TTT TTC TTT ATT TCT TTT TCT TTT TTT
2385 TTT TTT CTT TTT CTT TTT TTT TTG CAC ATG ACA GTG TTT GTA TTG
2430 AGG ACC TTC CAA GGA AAA GGG ATG CTG TAC CAG TGG TGC CTG GGT
2475 GCC TGG CCT CCA GTG TCC CAC CTC CTT CAC CAC CCC ACT TGG CTC
2520 CTT TGC CAT CTT GAT GCT GAG GTT TCC TGT TTG GTG AGA TCA GGT
2565 TGT TTG TGG TAA AAG AAA GGA AAG GGC TTC TGA TGG CTT TGC CAC
2610 AAG CTT ACC TGT GGG TTT CAG TCC TGA GAG GCC ACC ACC AGT TCC
2655 CAT CAG CAC TGT CTC CAT GCA GCA GTT GCT GGG TCC CAT GTC CAG
2700 CTG CCT CTT TGG CTT CAT GGG TTT TTC TGC TTC CTG CCC CCA CCC
2745 CCA CAT GTG CAA TCC TCA AGA TTT GTC CTG ATT CTA TTT CCT GGC
2790 ACC TCC CTG CCT GTC CTT GGG GAT TCT ACT TCT TCC TGT GTG GGG
2835 CCC ATA GCT GTT GTC TAA CAG GTA AGA AAT GAA ATT GAA CTA TTG
2880 ACT GGG CCC CAG AAA TCC ATA AAA TGG CTG CAG ACA GTT GTT TCT
2925 GTG TCC TGT TCT ACC CCC ACT CCA GTA CAT AAC TAC TAT GTA CTG
2970 TGT AGA GCC ATT CTA TAT GCT GAA TGT TCT GCT GTT GCA AAC TTG
3015 CCA GGG TAT TAG CCA GTG TTT GTG CCA AGC AGT TTT CGG GGA CAA
3060 CAG AAT GAC TCA GAC CAA GAT GGA TAG GAT GGT TAG GGC TTT GCT
3105 TCT TGC TGT TTT TCT TTG AAC TAG TCA TTG TCC TGC AGG TCC CTT
3150 CAT CTT CCA TAC CTA GCC CAC TCT TTT AGC CCT TAC CTT AAA TCT
3195 CTC AGA TAA GTT GGT TCA CAA AGA ATG TTA AGT ACT GAA TCA TGT
3240 GTG ACT GAG ACC AGA GAT GGC AAA TGA ATG GCA CAC CAT TTC TCC
3285 TTC TCC TGC CCC AGG GCA GGT ACC ACT GAT CTG CAT CAG AGT TGC
3330 CTG CTA TTC TCT GGT GTA TCC TTC ACA TCT AGG TGC CCT CAA GCA
3375 GCT GTG TGA GTG TTG AGA TCT CTG CCA TCT CTG GCT GAG ATA CTG
3420 CTG TCC TGT GAA GTG TTT CCC ATG ACC TTT TTC TTC CCC TTT GAA
3465 TCC CTC TTG TCT GGA GTA GTC CTT GCC TTC TTC TTG CTC CAG TAG

Fig. 17 (continued)

```
3510  GCC TTT TCC TTA CCC CAG CCC TTG TGC CAG GCT AAG CTG GTA CAA
3555  GAG CTG CCA ACT CAC AGA GTT TTG CTA GGC GAG AGA GGT GCA GGG
3600  AAG AGG CAG AGG TAT GCA CCT TCC CCC TTG AAG AGA GGG GAA AGG
3645  CCT ACA GTG GCC CAC ATA ATT GCC TGA CTC ACA CTT CAG CTA CCT
3690  CTT AAT GCC TGT GGA GGG ACT GGA GCT GCT GGA TCC CAG TGT GGT
3735  GGT GTA GGA GGC CAC AGT GAG CAG GTG GCC CCA GCT GGG TTT CCC
3780  AGG TCA GGA ATG TGG GCC CCA GGC AAG GTG CAG CCT TTG CTC ACA
3825  GCT CCA TCC ATG TCT AGA CCT TCA GGC CAG TCT GCA GAT GAG GTT
3870  CCC TAC CTT TTT CTT CTC TTC ATT GAC CAA ATC AAC CAA TCA CTA
3915  CAG CTG CTC TGC TTC TGC TTT CCA AAG TAG CCC AGG TCC TGG GCC
3960  AGA TGC AGG GGA GGT GCC TAT CCA TGA GTG AAG GCC AGT GTC TTC
4005  CTC ACC TGG GTG GTC CCA CAC TTG TGA CCC TCA GTT TTA GGA CCC
4050  AAG ATC TGT GTT GGT TTC TTA GAT TGC TAG CTT TTC CTC CAG GGG
4095  ACC ACA GCA GGT GAA GCT CAA GAG CGC ATG GCT CTG CTA ATA GTA
4140  AAT TGT TTT CAG GGC CTT GTC CAG CTG AGA GCT TCA TGT CCA CCA
4185  GAT TCT GAG AGG TGT CAG CAG CAC TTT TTT TTT TTA TTT GTT GTT
4230  TGT TTT CCA TGA GGT TAT CGG ACC ATG GGC TGA GCT CAG GCA CTT
4275  TCT GTA GGA GAC TGT TAT TTC TGT AAA GAT GGT TAT TTA ACC CTC
4320  CTC CAC CCC ATC ACG GTG GCC CTG AGG GCT GAC CCG GAG GCC AGT
4365  GGA GCT GCC TGG TGT CCA CGG GGG AGG GCC AAG GCC TGC TGA GCT
4410  GAT TCT CCA GCT GCT GCC CCA GCC TTT CCG CCT TGC ACA GCA CAG
4455  AGG TGG TCA CCC CAG GGA CAG CCA GGC ACC TGC TCC TCT TGC CCT
4500  TCC TGG GGG AAA GGA GCT GCC TTC TGT CCC TGT AAC TGC TTT CCT
4545  TAT GGC CCA ACC CGG CCA CTC AGA CTT GTT TGA AGC TGC ACT GGC
4590  AGC TTT TTT GTC TCC TTT GGG TAT TCA CAA CAG CCA GGG ACT TGA
4635  TTT TGA TGT ATT TTA AAC CAC ATT AAA TAA AGA GTC TGT TGC CTT
4680  AAA AAA AAA AAA AAA AAA
```

Fig. 18

```
GTG GAC GTG GAT GAG TAC GAC GAG AAC AAG TTC GTG
val asp val asp glu tyr asp glu asn lys phe val

GAC GAG GAA GAC GGC GGC GAC GGC
asp glu glu asp gly gly asp gly
```

Fig. 19

```
          1                                                   50
Rabbit    MSKNTVSSAR FRKVDVDEYD ENKFVDEEDG GDGQAGPDEG EVDSCLRQGN
Human     .......... .......... .......... .......... ..........

          51                                                  100
Rabbit    MTAALQAALK NPPINTRSQA VKDRAGSIVL KVLISFKAGD IEKAVQSLDR
Human     .......... ......K... .......... ........N. .........K

          101                                                 150
Rabbit    NGVDLLMKYI YKGFESPSDN SSAVLLQWHE KALAAGGVGS IVRVLTARKT
Human     .......... .......... ...M...... .......... ..........

          151
Rabbit    V
Human     .
```

Fig. 20

```
            1                                                   50
Rabbit      EERVLEKEEE EEEEEDDEDD DDDVVSEGSE VPESDRPAGA QHHQLNGGER
Human       .......... .DDD..EDEE ..-------- .......... .......-...

            51                                                  100
Rabbit      GPQTAKERAK EWSLCGPHPG QEEGRGPAAG SGTRQVFSMA ALSKEGGSAS
Human       ...S....V. ..TP....Q. .D......P. .......... .MN....T..

            101                                                 150
Rabbit      STTGPDSPSP VPLPPGKPAL PGADGTPFGC PAGRKEKPAD PVEWTVMDVV
Human       VA........ .......... .......... .P......S. ..........

            151                                                 200
Rabbit      EYFTEAGFPE QATAFQEQEI DGKSLLLMQR TDVLTGLSIR LGPALKIYEH
Human       .......... .......... .......... .......... ..........

            201                 220
Rabbit      HIKVLQQGHF EDDDPEGFLG
Human       .......... .....D....
```

Fig. 21

```
          1                                                   50
Rabbit    MKNQDKKNGA AKQPNPKSSP GQPEAGAEGA QGRPGRPAPA REAEG-ASSQ
Human     ---------- ------.... ......P... .E..SQA... V....PG...

          51                                                  100
Rabbit    APGRPEGAQA KTAQPGALCD VSEELSRQLE DILSTYCVDN NQGAPGEDGV
Human     ..RK...... R...S...R. .......... .......... ...G.....A

          101                                                 150
Rabbit    QGEPPEPEDA EKSRAYVARN GEPEPGTPVV NGEKETSKAE PGTEEIRTSD
Human     ....A..... ....T..... .....-.... Y....P..GD .N.....Q..

          151                                                 200
Rabbit    EVGDRDHRRP QEKKKAKGLG KEITLLMQTL NTLSTPEEKL AALCKKYAEL
Human     .......... .......... .......... .......... ..........

          201                                                 250
Rabbit    LEEHRNSQKQ MKLLQKKQSQ LVQEKDHLRG EHSKAILARS KLESLCRELQ
Human     .......... .......... .......... .....V.... ..........

          251                                                 300
Rabbit    RHNRSLKEEG VQRAREEEEK RKEVTSHFQM TLNDIQLQME QHNERNSKLR
Human     .......... .......... .........V .......... ..........

          301                                                 350
Rabbit    QENMELAERL KKLIEQYELR EEHIDKVFKH KDLQQQLVDA KLQQAQEMLK
Human     .......... .......... .......... .......... ..........

          351                                                 400
Rabbit    EAEERHQREK DFLLKEAVES QRMCELMKQQ ETHLKQQLAL YTEKFEEFQN
Human     .......... .......... .......... .......... ..........

          401                                                 450
Rabbit    TLSKSSEVFT TFKQEMEKMT KKIKKLEKET TMYRSRWESS NKALLEMAEE
Human     .......... .......... .......... .......... ..........

          451                                                 500
Rabbit    KTLRDKELEG LQVKIQRLEK LCRALQTERN DLNKRVQDLS AGGQGPVSDS
Human     ..V....... .......... .......... .......... .....SLT..

          501                                                 550
Rabbit    GPERRPEPAT TSKEQGVEGP GAQVPNSPRA TDASCCAGAP STEASGQTGP
Human     .....---- --------... ...A.S...V .E.P.YP... ..........

          551
Rabbit    QEPTTATA
Human     ....S.R.
```

Fig. 22 (1/5)

```
   1  AAGCTTTATAAAGATTTAACTACCTAATAAGGTAGAGAAGTAATTTATGTGCCCACTAAA   60
  61  AAATACTCAATTTCTGAATGTTCGTCCAAAATTAACTTGTCAGATCATTAAATCATTGAC  120
 121  TAGAAACACGTTGAGTACCTATTATGTACTAGGCACTTAGATCATTGTGAGACAATAAAA  180
 181  AATACTGCATTAGAAAAGGACATTTTTCACATCTTAAATGCAATAAGCATTATTTGGCTG  240
 241  GCAGTTAATTACATTTAACACATTAAACATATAGAGCAAAATTCTGAGCAATCAAAATAA  300
 301  TTATACCCTTGAGCAATCGATTATTTAAATTTCTTTCACTATTCCCTTAAGCTGATTTCT  360
 361  ACTCTGGGATTCTTTCATAGTTCTCAAATAAGAAAATAAAAAATTTCCTAAATAAGGCAA  420
 421  TACAAAAGAATAGAAATGTAAGAGAAGAGATATATTAGCTCTTGAATCCCTGTTTCCATT  480
 481  TGCTGTCAATAGTGCCTCTAATGTTCGATTTTCTCTTCAAAGAAAAATCTTGATTTAAAA  540
 541  GGAAGAAAAAGTACAATCACCTTTAACAGCTAAAGTATACTGATTAGCATCTACTAAAGT  600
 601  TAGCAAAGACTGAAACTGAAAAAAAATTGTAAAATCTTTATTCTAAGTTATATAACGCCA  660
 661  TTCACCATAGTAATGATTTTATACTTTGGTATATGGCTTTTTAAAATAAATATTGCCAAC  720
 721  AGGTAAAAATTTTTCCTTTGCTGTCTTAAGGCATTCCTAAGAGAATTTTTACCAGTGTGT  780
 781  GTTCATAACTTGAATGTTAATTTAAACAATGTTACTTCTATCACCTAAATGATATACTTA  840
 841  TAGAAGAGTGGTTTAATTGGGAACAGAAAAACACCACATTGCTTCTTCCCAAGAAAAAGG  900
 901  GATGTATTCCATTCTCGAGGTCTCTCTCCCACTCTCTATTTATATATAATATACTGCATA  960
 961  GATAAATATACACACATTATATATGTATTTTTTTGAACTTAAAGAAGACTGGACATATGT 1020
1021  ATTTACATGTATATATCCAACAAATATTTAATTTTGAGATCTCTCTCCCTCTTCTGATTT 1080
1081  ATTATTCTCAGTATGAATTCTCAAACTGTACGGTCTTTCACATTTCATTCATTCATCAAG 1140
1141  CATGTATCGAGTCCCTTCTGCATGCTTAGCTTTTTGTCATATGGAAGGAAGATACAAAAG 1200
1201  AAAAACTGTTTCTGCCCTTCAGAATCTTTCCATCTCTTCTAGGAAGGAGATAAAACACCA 1260
1261  TATATCATTAAGAAATTTATAAGACTAGTCCCAAAACCAATGGTACAAGCAACATGCATT 1320
1321  TTACATTTATGTAGAATTTTAGAGCTTGGAAACACTTTCGTGATATATAATCCTAAGAAC 1380
1381  AATCTTGTAAAGTGCACATTATTAGCTCCATTTCAGTGATGAGGAATCTGAGACAGAATT 1440
1441  TTAAGTGACATGTCTCGTTCAAACATTATGAGTGGAAGAGTCAACACTTAAGCCTGAGTT 1500
1501  TTCTGATTCTAAGCCTAGTGCTCTTTTCAACACAGCACTGGAAACCAAAGATTGTGGTAC 1560
1561  ACAACAAGGCAACAGCCAGTCTTCTTGCTCGAGGTCCAACTAAACTGGACCCATACCGAG 1620
1621  CAGTGTCCAGCCAAATGTCCAAATTAATTTTATCCTGCAAATATTTGTTCTTCAGTGTAA 1680
1681  TACACACAGCACAACTACCATTTCCTTCGTCTTAGTGCCTTTATCTCCTACATTCCAGAA 1740
1741  ATGGGGATGTCAAATATTTTTTTAAATCTGGCCTAGATGGAATCATATAAATCTCAAATC 1800
1801  ATAATATAAATCTTAAAGGTCTGGTTTCCACCAATCCTTCCACATTTTGTTTTCCCCCAG 1860
1861  CACTAGAGAGCCTAACCTACCCTCACCCCTTTCGAGCATTCTTGCTCCAAACGACCACCT 1920
1921  ATTTTAAGATGTCAATGACCCTTTCCCAAATTCTACAAATTCACCCCAGTTTTGCCACCC 1980
1981  GACCCCAGCGCCTGCCCGGACACGTTCCCCTCCCTCCCAATAGATTTGATACCGAGTTCA 2040
2041  GGTTCTGCAGATCCCGTTGCGATGCTGTCACACAGCACTGACAGATAAGATTTGACCTTT 2100
2101  CGACTCCGTCCTTGGGGACTTCCCGCTGGCCAAGAAGGGTAGTTCCAATCCCAGGAAACG 2160
2161  GGCTTCCTGCTCAGGAACGCAGCCTCTAGCAGCGCACAGTCTGAGGCAATGTCTCCGGCA 2220
2221  ATTAGAACGATGCTGGGCGCCCGGGTGTGCATCACTCTGCCTCATACTCCTACCAACTGC 2280
2281  AGGGCACTCGGTCCGGCAGCCAGTCCATCCCACCCACACCCAAGTCCCAGCCAGCCGGAC 2340
2341  CTTACGCAGGACCCCGATGATAGGTCGTTGACGGCTGCAGCAAAAGCCAAGGCCACCTGC 2400
2401  CGCTGCTGCCCATCCCCGCCAATCTGAGACCCCCTAGACTGGACCGCAGAAAAGCGTTTC 2460
2461  TATGGGAACCCCCCCACCGAGAATCACGTGACGCAATCGGACGACCAATCGCTTCTTACC 2520
2521  TCTGCCCGCGGTCCAGCTTTTGGCCCTCCCTCTCGCCCCCGCCTCCTTCGCCCAGCCCCG 2580
2581  CCCCTTGCCTGCGGAGAGCCCGCGCCTGCGCGCTGTGTCCTGCGCGCTCCTTCCCTCGCG 2640
2641  CGCGCTCTCCGTGGAAGAGCAGGGGCAGCGTGGGAGGCGCCAAGGGAGCGCGAACCTGAG 2700
2701  GAGGAAGAAACGGGGCTAGCGCGCAGGCCCAGAACGGTCCGAGCCGCGGCAGTCGGCGAC 2760
2761  GCCTCAGAGCGGAAGAGGGAAGTGAATCAGGCGCCGGGTAGTGGGTTGCTGGGCTGGGCT 2820

2821  TGCTGAGGTAGAGGCAGCGCCAAGAAGAGGCCTTTGCCGCTGGTCGGGATTGGGATGTCG 2880
                                                      M  S

2881  AAGAACACAGTGTCGTCGGCCCGCTTCCGGAAGGTGGACGTGGATGAATATGACGAGAAC 2940
      K  N  T  V  S  S  A  R  F  R  K  V  D  V  D  E  Y  D  E  N
```

Fig. 22 (continued; 2/5)

```
2941  AAGTTCGTGGACGAAGAAGATGGGGGCGACGGCCAGGCCGGGCCCGACGAGGGCGAGGTG  3000
      K  F  V  D  E  E  D  G  G  D  G  Q  A  G  P  D  E  G  E  V

3001  GACTCCTGCCTGCGGCAATATCCTTGCATTCACCGCCCTCCCCACCCCAGCCCAGCCCAG  3060
      D  S  C  L  R  Q

3061  CCCGCCCTTCTCCTGGGACCCGGGAGCCTGCAGGATCCGCGGGGCACCGGCGCGGAGCTG  3120
3121  CCTCTCAACCTGCGGCTTAACCTGTCTCTTTGGGATCGCCCGCTCTGAGAGGGCAAGGGG  3180
3181  GAAGCCCCCGTTTCCTACCCAGTCGGCAGGAGACGCGAGGGTCCCACTCTTGGAAGCCTG  3240
3241  CCCTACCCCGCGCGCCTTCCACGCCCCCAGATTCCTCAGGTTGCACCCGAGTGCCTGCCT  3300
3301  GCCTCGGGAACTGGTCCCGCCGCCCCGCGCCCTCGCGGCGCTGGGGAAGGCGGCCCCGGCT  3360
3361  GGTGGGGAAGGCTGGTGCCGACCGCCTTAGTTTTTCTTCCTAGAACTCTGATTTCCTGGG  3420
3421  GTCACATTAGCTCCAGAAATTTCTGATTGTGGGGAACCTGCATCTTTCCTTAGTGGTTTT  3480
3481  GTTTTTTGGTTGTGTTTTTGTTATTGGTAGCGTTAAGGTAGTTTATTGCTTACCGGGGGG  3540
3541  CCGGGGGAGATGGGACTGTTCGAAAATTGAGGGTCCCTGTGCTTTCAGCCCATTGGCCTT  3600
3601  TTTAAAAAAAAAAAAAAAAGAAGAAGAAGAAGGGGATTTGGCAAAATATACATTGTACAG  3660
3661  AATTTGTTAACTGGGGGAGGGGAATGAATACAAAAAATACAAAACTCCTAGAAGGAAGCT  3720
3721  TGGAGCCTTTTACCTGCTAAGAAAAGGACAATAGAAAAAACAACGGGGAATGCGTGTGGA  3780
3781  GAATCCTTGGAAATATTTAAAATAAACCCCAATGAATAAGATAGAAGATGAGTCATTCGT  3840
3841  ATAAAGCAGAATCATTTTTGTAATCCTAAAATTGTTTCCATTTTAGTTAAAATATGGCAG  3900
3901  TCAGTTCCCGGTTTCTGTTTTTGCATATTTGAATATTCATAACTTTGGCTTCGCATTTGC  3960
3961  ATTACATCTTTTTTAGAAAAATGTAAATGTTGCAAAAAAACCGAAGCTGTAGTTTTAGAA  4020
4021  AATCTCAGACACTGAATTTGTATGCATTTCTAATTCTTGGGTGTATTCATAAGGAAGACT  4080
4081  CTCAACAATGTCCTGTTATAGTGGGGAAATATGAGAGTGAAAATATTTAATGGCAACAAT  4140
4141  ATCCTTTTTTAAAGGCACCTAAATAGAGCATTAGACATTTATCAATATATAGATAGTGCT  4200
4201  TTGCCCAACTTTCACAATTAATTAGCTGTTGCTCTTTTGCATTATTTAAATACTTAAGTG  4260
4261  CTTGGAGTTATAAAAAATGAGCTAATCTACATCAGGCATGCTTCTCTAGAAATCCCTGCA  4320
4321  GCCTTGAAAATAACAGCTTGTCAACCAGAGATTTTGTGTAAGAACTTTTTCTTTAGAAAA  4380
4381  TAAATGGTGAACATGCTTCCTAAAAACATTATTTGTGATGGGATAAGATGGTGTTTTATG  4440
4441  AAACCCCAGTGTATTTTAGGTAATTTGTGGTGACTTTTAAAAGGTACTGCTGTATCCATA  4500
4501  TCAGTGGATCTGCTTTTTGATCAGTTCATCTTAAAATATAAAGATACTGTCTCTTCTTAC  4560
4561  CGTTACATACAGCCAGGAAAGACAGCCCTAGTGGTGGGGTACTAGAGTTGGAGGAACAAG  4620
4621  TGAACTCTGTGGTTTTCCTTTTAGGGGAATGTTTGTACATTCTGACAGTCTGATTGGCCT  4680
4681  TCTGTTTCTCATGCTTGCTAACTCACTAGTGCTTTCAAAGAGAGCCTGAATTTAATAGGT  4740
4741  ATGGTCTAACACAGTTTGAATAACCTTTGTGAAATATGAGAGAAAATATCTAAAGCAAAA  4800
4801  AATTAAGCTGCCACCTAAGGGACATATGAATTATTACATCTTCTGTGATGCCTCTTTTCA  4860
4861  TCAATATTGAGAGATTGCTAATGTGTATCATTCAGATTGCTAATCTGCCAGCATGTTCTA  4920
4921  CCAGCATTTCAGATAATACAGAATATGGTTCTAGCAAAAGTTTGGTCTTTATTTTTTCAA  4980
4981  TTAGAATCACAGGAAAAGACATATTTTGGTTGATAATAGGTTATTTCATTTGGGGGACTA  5040
5041  ATAATTCTGATATATATTTTAGGATTTCTTTAACACCACTCTAGGTAATGTTTGCATATG  5100
5101  TATCTCACTGGGAAATGAAAGACTATCAAGGTGTTCACTTGATAGTTAGAACCAAGGGTG  5160
5161  AAACAGTCTTTGCTTTATTAAAAAAAAGTCTAATGTTCTATTTTGCTTTTGATATTTTGC  5220
5221  CTTTGATTAACATCCTGGAAACCAACACATTGAATTTCCAGTATTGAACATAGTGACCAA  5280
5281  AGTAATTTTCTTTTTATATGTAAATCAAGTCATAAAGAACCAGTGGTTATAATGCTTTCT  5340

5341  GGGGGCCATCCTTTGCTGTTACACCCTTAACTTCCATCACAGGAAACATGACAGCTGCCC  5400
                                                  G  N  M  T  A  A  L

5401  TACAGGCAGCTCTGAAGAACCCCCCTATCAACACCAAGAGTCAGGCAGTGAAGGTGAGTC  5460
        Q  A  A  L  K  N  P  P  I  N  T  K  S  Q  A  V  K
```

Fig. 22 (continued; 3/5)

```
5461  GCAGACTACAACACAGTGATCTCTGCTGATATCTTATTCTTAGTAAAATCCTTGCAGTGC  5520
5521  AAAAAAAAATCAATATTTTAACTGTTTGCTATCTTTGACAAGAAGAGTTTATAATGTAGT  5580
5581  TTGATAGGTAAAAATTTCACGTGAAAAAATAGCCCTATAATGTAGTTATGATAATGCTGC  5640
5641  ATGGTAAGATACAGTAAGTTCAAACGATAGTGAAATCATTTGTGTGTGTTTTTAGAGGAG  5700
5701  ACCACTCAGGCTGAATTTGAGCAAAGGTTTGAAAAATAAGTTAAACCTTTACAAAAATAA  5760
5761  ACAGATTGTAATTGCTTTTTAAAGATTTTTTAAAACCATACAAATACTAAATACTTATTA  5820
5821  TAGAAAGCTCAGACATATGAGAAGGTTAAAAAGATAGTGGTTTGTGGTCCCAGCACCCAG  5880
5881  AGATAACAGTTACTACTTTGGGGCCTTGCTGTATTGTTACAGAGTTCCCTTTTGTTTTTT  5940
5941  TAAGAATGAATTTTTAAAACGGGCTTTTTCAGCTATATGCAATGGTACATGAGCTTTCCT  6000
6001  TCCCCAATAAGTTAATAGCCTTTTTTAACACTTGTATATGGATAAGCTCCAGTGTATACA  6060
6061  TAACTAATCTTTTGTTTATATTTAGACTGACTTTTTTTTTCCTATTGTAAACCACTGAAA  6120
6121  TCAATATTTTTTGGTAAATTTTTAATTGTTCTCTTTGAGTAAATTGCTAGCAGTGAATTA  6180
6181  CTGGATCAAAGAATGCACTTTTTTTTAAGGCTTTTGGTATGCAGTATTGCCAAATTGCCC  6240
6241  TTCAGAACAGTTGTGCAACTTACATTCTCTGCAGTCTTTTACTAATTCTTAACCTATTTA  6300
6301  CGTATTTATTTAAAATGATGCCCATAGCATCAACCCCGTTGTCCATAGCTATTCATACAT  6360
6361  CCTAGGAGCTTCAAGAATCTCAATTGAATAGTAGTAAGTAATAACTTAGGTAAATGCATA  6420
6421  ATAATTATCTAGGTAACATAATTTTTTATTGGGGAAAATTTCTTTGGTTTTTACAAGTTG  6480
6481  TAAAGATTGTCGTTGAAATTTCATTTTTACCGTGGATGCAAAGATATTTTTCTAAATCTG  6540
6541  GTAATTGCAGTCTTTAAACCAAAGATAACAGTAGGTGGTAGAAACATTCTGTGAAATCCT  6600
6601  GACCAGTAGGAATGCTGGAGGTATCACTTTGTGTTGAATGGAAGGAGAAACGAATTGTTG  6660
6661  AAAAGGTCAGTTAAGTGTTTCCTTTGCTTGGCCGGATGGGTAAGAAAATAACTGCTTTTG  6720
6721  AAGCAGGCTTTTGCCAAAGAAAAAAGATCATTATTAATGAACATCACTATATTTCATATC  6780
6781  TACAGTCAATTCATATAAATTACAGTCAATTTTCTTTTAAGACAGCTTGGTTTATTAAAA  6840
6841  TTTTTAAATAAAAAAGTTTTTAAGAAAAAATTACTTCTGAAGGATAATTCAAGGTGAAAC  6900
6901  TGCAAATCTGCCTCCTTGTTTTGTTGGGAATTTTTTTTTTTTTTTTTTTTTTGAGACG  6960
6961  GAGTCTCACTCTATCACCCAGGTTGGAGTGCAGTGGTGCAATCTCAACTCACTGCACCCT  7020
7021  CCGCCTCCCGGGTTTAAGCAATCCTCCTGCTTCAGCCTCCCGAGTAGCTGGGATCACAGG  7080
7081  CACACACCACCATGCCTGGATAATTTCTGTATTTTTAGAAGAAAACAGGGTTTTACCATT  7140
7141  TTGGCCAGGCTGGTCTCGAACTCCTGACCTCAGGTGATCTGCCCATCTCGGCCTCCCAAA  7200
7201  GTGCTGGGATTACAGCTGTGGGCCACCACACCCGGCCGTTTTGTTGGGATTTTTTTTTTT  7260
7261  TAAGATCAAGACATAAATTTAAATGTTGTTTTAATAAATTGTTAAATTATCACATTGATC  7320
7321  TGTTAGCAAATCCTCTCAGCTCTGCCTTCAATTATGTTAATAGTCTGTCAAGTTTCTTAC  7380
7381  CACCTCCACTGCTACTATGCTTACCACATCCAGCCTGTATTATTGCAATTGCCTCCTAAT  7440
7441  TGCTCTCCCTGCTTCTACCTTATCCCCTACTCCCACAGCTTATTTTCTGTAACATAGATG  7500
7501  CCAAAGCAATCCTGTTAAAATGTGAGTCAGATTATGGCACTGCTCTTAAAACCTTCCAAT  7560
7561  GTCTTCTCATTTCTCTCAGTAAAAGCCAAACTCCTTACAATGCCTGTAGGCCTTACACGA  7620
7621  TCTGTCCTCCCATAACCTCTGACTTACTCACGTGCTTTTCTCCCACCAATCCACTCCAAC  7680
7681  CACATTGGGTTTTTTTCTGTTCCTGGAACACACTGAACACACACTAATAGCACTGTTCTT  7740
7741  TCCTCTGTCTGAAACACTTTCCTCAGTTATCCCAAGCCTTCTTTCACGTCCTTCAGGTCC  7800
7801  TTACTCAAATGTCACATTCATAGTGTAGACTTTCTGAAATTCTAAACCCTCCTCATACAG  7860

7861  ATATGTCTAAATGTTCTGTTATTTATTGACCCACCAGGACCGGGCAGGCAGCATTGTCTT  7920
                                          D  R  A  G  S  I  V  L

7921  GAAGGTGCTCATCTCTTTTAAAGCTAATGATATAGAAAAGGCAGTTCAATCTCTGGACAA  7980
       K  V  L  I  S  F  K  A  N  D  I  E  K  A  V  Q  S  L  D  K

7981  GAATGGTGTGGATCTCCTAATGAAGTATATTTATAAAGGATTTGAGAGCCCGTCTGACAA  8040
       N  G  V  D  L  L  M  K  Y  I  Y  K  G  F  E  S  P  S  D  N

8041  TAGCAGTGCTATGTTACTGCAATGGCATGAAAAGGTAAGTTATGAATTATAAATCTATAT  8100
       S  S  A  M  L  L  Q  W  H  E  K
```

Fig. 22 (continued; 4/5)

```
8101   GACTGGTTCTTTTACAATAGGGAATGACAATGACAACCTCTCTCACCTAAATAACCATTT   8160
8161   TGATTTGTTGTACATTTTTGTTATTACAAATAAAATGCATGAAAAGGATAGTTCATATTT   8220
8221   ATGTTTACTAGCCTTGGTCTTAAGAGATTCTGATTCCAACACTTGTGTTTATTCAACAAT   8280
8281   GATTATTAGTAATTAAACATAATCTTGAACTCTGAATTAAATCAAAACTTTGTAAAAGAA   8340
8341   AATAAGCAATACAAATCAAGAATTCTTTCACAGTGACCAAAAGGTGAAAACAACACAAGG   8400
8401   ATCGAATATGATTCAACCA                                           8419
8420   TTAAAAGGAATGACATTCTGACACATGCTATAACATTAATAAACCTTGAAAACATACCAA   8479
8480   GTGAAATGAGCCAAACACAAAAGAACTAATATTTTATAATTTTACTTATATGAAATAATC   8539
8540   TAGGATAGGCAAACACAAAGGGACAGAAAGTCCTTAGAGGTTACTAGGAAGTAGGGAAAG   8599
8600   CAAGGAATAGGGAGTTAGTGCTTAATAGGTACAGAGTTCCTCCTTGGAGTGGTAAAAAAG   8659
8660   TTTTGGAAACAGATAGTGGTGATGGCTACAGTACATTGTGAATATAATTAATGCCAATGG   8719
8720   ATTTTACACTTAAAGATGGTTAAAATGGCAAATTTTGTGTTAGATATTTTACAACTTTTT   8779
8780   TAAAGAATTAGGAGTTTGGAGGATCAAGAATTCTTAAATCATGTTTTTCTATTTTCATGT   8839
8840   GTATATTTTGCAATGTAAGTAGATGCTGGTACATCATCTGTCAAAAGAGTATAAGTGATT   8899
8900   TTGAGCTTTGGGTAAAAAACTGGATAACATGTAAATAGAACCAGTCATAAAAATATTGAG   8959
8960   TGTTTGAAGTGTATCTGAGTGAAAACACAAACATAAGAAAAAAGCACATAGTAAAACAAT   9019
9020   AGTTCCCCCTTTTACTCTAAAATGCACCAATTTGGGTAGTAATTTATATGGCACCCTATT   9079
9080   CATGGAACACTTTCTGTTGCCAGGTACCATACTATTAATGTTTTATTTAACCTTTACAAC   9139
9140   AACCCTGTGGAAGTATATAAATATCTTTATCATCCTCAATTTACAGATGAAAAGCTAGCT   9199
9200   TTAAAACCCAAGCCAGCGTAGTTCTAGCATAGCCTCAAGATTGCAGTGAACATTGATTAC   9259
9260   TTATTATATTCCACATATTCTTCAAAGGACTTTATAAATATTAACTCATTTAATCCTCAT   9319
9320   AAAAATGGAGGGAAATGCTTGCTATTATTCCTCTTTTGTCACTGAGGAAACTGAGGCATG   9379
9380   TGTGAAGTCTTCATTTCTTCCAAATGTCAGTCACCAGTTTTTACCAATCTTCGAAGTATT   9439
9440   TCTGAAATCTATCTGTTCAAGCGTATCTAATGCAGCTGTTCACAGCATCTCTCCCAGTCT   9499
9500   GTTGCCATAGCTTCCTGACTGGTTTCCCAGTTAACAGTTTTGCCTCCTTCAAATCTGTTC   9559
9560   TCCACCCAGCCATCAAAATGATATCTTTAAAATCAAAATTGCCCTTGTCAGTCACCTGCA   9619
9620   GGGATAAAGTCAAAGTTCCCAAGTCTAGCTTCATCTTCCATGTCATTCTTCCCCTCAGGC   9679
9680   TATAGCAATGCCAGCCTTTTTCCTGAATGCACCATATTGTTTCACACCTCCATACATTTG   9739
9740   CTCATGATTTTCTGGTGTTAGCCTGTCACCTACTCATTCTTTTAATGTGTCATTTCCTCC   9799
9800   ATGAAGCCTTAGCTGAAACATTCCTCTATACTGTTAATCTGGGTATAAGCCTCTCCCTGG   9859
9860   TGCTTTAATAGCACCTGCAGCACAACTCTCATTTCATACATTAGATTAAAATTACCTGTT   9919
9920   TATATGTCTGTCTCCTCATGCTAGACCAGAAAATGCTGTATTTGTTCACTTTTGTATCCC   9979
9980   CAGCATCTAGCACAGTACTCAGTATACAAAGGTATTCCATAAATATTTTTTGAACAGAAA  10039
10040  GAAACCAGAGCTCAGATTCCTAATACTTGATCATTACTCTCTATTTTTCAAATTAGAGTC  10099
10100  AGAGTTAAAGTTTCTAAGTTCTTAGCTATTAAACAATACCTTCTTTCTTTGGGAGAAAAA  10159
10160  AAATCTGACAAAGGCTGACTAATCGAAGTGGAAGTTGGGATGGTTGATCCCAGTTTGAAT  10219
10220  TTTCTTCTGACTATGTGGTGAGAATGAGAAATGCAGAATGTCCACCTGTTTTGAGCAGGA  10279
10280  ACACTATGCTGCAGATTTTTTTTTTTTTTTTTTTTTTTTTTTTTGAGACGGAGTCTTGC  10339
10340  TCTGTCGCCCAGGCTGGAGTGCAGTGGCGCAATCTCGGCTCACTGCAAGCTCCGCCTCCT  10399
10400  GGGTTCACACCATTGTCCTGCCTCAGCCTCCCGAGTAGCTGGGACTACAGGCACCCGCCA  10459
10460  CCACGCCCGGCTAATTTTTTGTATTTTTAGTAGAGACGGGGTTTCACCATGTTAGCCAGG  10519
10520  ATGGTCTTGATCTCCTGACCTCGTGATCCGCCGGCCTCGGCCTCCCAAAGTGCTGGGATT  10579
10580  ACAGGCGTGAGCCACCGCGCCCGGCCTATGCTGCAGATTTTTTAAAACATTATTTAGAAT  10639
10640  TAATGTACTAAAATGTAAACTAGTATCTCACTAGAATGTAACTTCATGAGGGCAGGGACT  10699
10700  TTCAAGGTTTTGTTTATTACTGTAACCTCAGTGCCAAGAACAGTACCTGGTGCATAATTG  10759
10760  GTGCTCAAGAATTTATTATTTGTTAACTAATAAATTCAGGGTCTATAGCAGTGCCCATTC  10819
10820  CTTCTTTAAGAAAAATGTTTTACCAAATATGAGAATTGACCTTTTATTATTCTGTCAACA  10879

10880  TTTACATCCTGGTTTGTTTTTAGGCACTTGCTGCTGGAGGAGTAGGGTCCATTGTTCGTG  10939
                              A  L  A  A  G  G  V  G  S  I  V  R  V

10940  TCTTGACTGCAAGAAAAACTGTGTAGTCTGGCAGGAAGTGGATTATCTGCCTCGGGAGTG  10999
         L  T  A  R  K  T  V  *
```

Fig. 22 (continued; 5/5)

11000 GGAATTGCTGGTACAAAGACCAAAACAACCAAATGCCACCGCTGCCCTGTGGGTAGCATC 11059
11060 TGTTTCTCTCAGCTTTGCCTTCTTGCTTTTTCATATCTGTAAAGAAAAAAATTACATATC 11119
11120 AGTTGTCCTTTAATGAAAATTGGGATAATATAGAAGAAATTGTGTTAAAATAGAAGTGTT 11179
11180 TCATCCTTTCAAAACCATTTCAGTGATGTTTATACCAATCTGTATATAGTATAATTTACA 11239
11240 TTCAAGTTTAATTGTGCAACTTTTAACCCCTGTTGGCTGGTTTTTTGTTCTGTTTTGTTT 11299
11300 TGTATTATTTTTAACTAATACTGAGAGATTTGGTCAGAATTTGAGGCCAGTTTCCTAGCT 11359
11360 CATTGCTAGTCAGGGAAATGATATTTATAAAAAATATGAGAGACTGGCAGCTATTAACAT 11419
11420 TGCAAAACTGGACCATATTTCCCTTATTTAATAAGCAAAATATGTTTTTGGAATAAGTGG 11479
11480 TGGGTGAATACCACTGCTAAGTTATAGCTTTGTTTTTGCTTGCCTCCTGATTATCTGTAC 11539
11540 TGTGGGTTTAAGTATGCTACTTTCTCTCAGCATCCAATAATCATGGCCCCTCAATTTATT 11599
11600 TGTGGTCACCCAGGGTTCAGAGCAAGAAGTCTTGCTTTATACAAATGTATCCATAAAATA 11659
11660 TCAGAGCTTGTTGGGCATGAACATCAAACTTTTGTTCCACTAATATGGCTCTGTTTGGAA 11719
11720 AAAACTGCAAATCAGAAAGAATGATTTGCAGAAAGAAAGAAAAACTATGGTGTAATTTAA 11779
11780 ACTCTGGGCAGCCTCTGAATGAAATGCTACTTTCTTTAGAAATATAATAGCTGCCTTAGA 11839
11840 CATTATGAGGTATACAACTAGTATTTAAGATACCATTTAATATGCCCCGTAAATGTCTTC 11899
11900 AGTGTTCTTCAGGGTAGTTGGGATCTCAAAAGATTTGGTTCAGATCCAAACAAATACACA 11959
11960 TTCTGTGTTTTAGCTCAGTGTTTTCTAAAAAAAGAAACTGCCACACAGCAAAAAAATTGTT 12019
12020 TACTTTGTTGGACAAACCAAATCAGTTCTCAAAAAATGACCGGTGCTTATAAAAAGTTAT 12079
12080 AAATATCGAGTAGCTCTAAAACAAACCACCTGACCAAGAGGGAAGTGAGCTTGTGCTTAG 12139
12140 TATTTACATTGGATGCCAGTTTTGTAATCACTGACTTATGTGCAAACTGGTGCAGAAATT 12199
12200 CTATAAACTCTTTGCTGTTTTTGATACCTGCTTTTTGTTTCATTTTGTTTTGTTTTGTAA 12259
12260 AAATGATAAAACTTCAGAAAATAAAATGTCAGTGTTGAATAATTTATTTTTCTCTGACAC 12319
12320 TTTAACAATTATGAATGTATGGTTAATTAAGAGGAAAGGTTTTCTGCTTCTACCACCAAG 12379
12380 TACTGTACTCTTAACAAGAACAGTTTGGTAGGGTTTTTATAAGACTATATAGATATAAGA 12439
12440 TGATAGAGAAGAGAGTCATGAATGATGTCAGAGCACTACTGAAGCCTTTGGAGTGATTCC 12499
12500 ATAGCCTTCTGGATGGCAGCTGAATACCTATATGTAGTATCACTGCCCAAAGACCTAGAC 12559
12560 TAGAAAGTGCAAAGTAGCTTAGCAGCTGCAGTCATTCACTCCCAGCCTCCAAAATTCTCT 12619

Fig. 23 (1/6)

```
   1 -                                          GATCCCTCTCCAGGTGGAAG - 60    /|\
  61 - CTCCCTTCATACCAAAGTTTAAAGGCCCTGGGGATACGAGTAACTTTGACGACTATGAGG - 120    |
 121 - AAGAAGAAATCCGGGTCTCCATCAATGAGAAGTGTGGCAAGGAGTTTTCTGAGTTTTAGG - 180    |
 181 - GGCATGCCTGTGCCCCCATGGGTTTTCTTTTTTCTTTTTTCTTTTTTTTGGTCGGGGGGG - 240    |
 241 - TGGGAGGGTTGGATTGAACAGCCAGAGGGCCCCAGAGTTCCTTGCATCTAATTTCACCCC - 300    |
 301 - CACCCCACCCTCCAGGGTTAGGGGGAGCAGGAAGCCCAGATAATCAGAGGGACAGAAACA - 360    |
 361 - CCAGCTGCTCCCCCTCATCCCCTTCACCCTCCTGCCCCCTCTCCCACTTTTCCCTTCCTC - 420    |
 421 - TTTCCCCACAGCCCCCCAGCCCCTCAGCCCTCCCAGCCCACTTCTGCCTGTTTTAAACGA - 480    |
 481 - GTTTCTCAACTCCAGTCAGACCAGGTCTTGCTGGTGTATCCAGGGACAGGGTATGGAAAG - 540    |
 541 - AGGGGCTCACGCTTAACTCCAGCCCCCACCCACACCCCCATCCCACCCAACCACAGGCCC - 600    |
                                          Human cAMP-dependent protein kinase
                                          catalytic subunit alpha
                                          Accession number X07767 (until *)
                                        - follow arrow until line that
                                          begins 1561 -
 601 - CACTTGCTAAGGGCAAATGAACGAAGCGCCAACCTTCCTTTCGGAGTAATCCTGCCTGGG - 660    |
 661 - AAGGAGAGATTTTTAGTGACATGTTCAGTGGGTTGCTTGCTAGAATTTTTTTAAAAAAAC - 720    |
 721 - AACAATTTAAAATCTTATTTAAGTTCCACCAGTGCCTCCCTCCCTCCTTCCTCTACTCCC - 780    |
 781 - ACCCCTCCCATGTCCCCCCATTCCTCAAATCCATTTTAAAGAGAAGCAGACTGACTTTGG - 840    |
 841 - AAAGGGAGGCGCTGGGGTTTGAACCTCCCCGCTGCTAATCTCCCCTGGGCCCCTCCCCGG - 900    |
 901 - GGAATCCTCTCTGCCAATCCTGCGAGGGTCTAGGCCCCTTTAGGAAGCCTCCGCTCTCTT - 960    |
 961 - TTTCCCCAACAGACCTGTCTTCACCCTTGGGCTTTGAAAGCCAGACAAAGCAGCTGCCCC - 1020   |
1021 - TCTCCCTGCCAAAGAGGAGTCATCCCCCAAAAAGACAGAGGGGGAGCCCCAAGCCCAAGT - 1080   |
1081 - CTTTCCTCCCAGCAGCGTTTCCCCCCAACTCCTTAATTTTATTCTCCGCTAGATTTTAAC - 1140   |
1141 - GTCCAGCCTTCCCTCAGCTGAGTGGGGAGGGCATCCCTGCAAAAGGGAACAGAAGAGGCC - 1200   |
1201 - AAGTCCCCCCAAGCCACGGCCCGGGGTTCAAGGCTAGAGCTGCTGGGGAGGGGCTGCCTG - 1260   |
1261 - TTTTACTCACCCACCAGCTTCCGCCTCCCCCATCCTGGGCGCCCCTCCTCCAGCTTAGCT - 1320   |
1321 - GTCAGCTGTCCATCACCTCTCCCCCACTTTCTCATTTGTGCTTTTTTCTCTCGTAATAGA - 1380   |
1381 - AAAGTGGGGAGCCGCTGGGGAGCCACCCCATTCATCCCCGTATTTCCCCCTCTCATAACT - 1440   |
1441 - TCTCCCCATCCCAGGAGGAGTTCTCAGGCCTGGGGTGGGGCCCCGGGTGGGTGCGGGGGC - 1500   |
1501 - GATTCAACCTGTGTGCTGCGAAGGACGAGACTTCCTCTTGAACAGTGTGCTGTTGTAAAC - 1560   |
1561 - ATATTTGAAAACTATTACCAATAAAGTTTTGTT*TAAAAAAAAAGTGTCGCTGGTGTTCTC - 1620 |
1621 - GACTTCGATCACCCACCCACACACCCCCAGGGGGTTGGAAAGGGAATTTCGGACCCCAGC - 1680
1681 - GTGCAGGCCGATCAGGTCCTGGCTTGAAGTCCTTGTAACCAGGGTTTAGCTGAAATTCCG - 1740
1741 - GCACTCCTTCGGCCCCGCAGGAGAAACGAGCGTCAAACTGCCCTTTGACCCCAGATTCGG - 1800
1801 - GGTCCCCAAATCTGCGGCGCGCCCCCTCGGCGTCCAGCCCGGGACCGAGAGGGCGCTCTA - 1860
1861 - GGGAGGCGCTGGGGCTGGCGCGCCAGGAGGCCGAGCGGCGGCGGGGGCGGCCCTGGCAGG - 1920
1921 - GGGAGTAGAAGGGGGAGAGGGTGCGCGCCCCCCTTCCCGCATCCTCAGCGCCGGGCCAGG - 1980
1981 - CGCGCCTGAGGGACGCGGGGGCGGCGGCAGCAGGAGGGTCCCCGCAGCACCCTGCGAGCG - 2040
2041 - CGGCAGCCCCGGCCCGCGGGCGGCGAGTTCCCGGTAAGTGCGGTCCCGAGAGCGGAGCGC - 2100
2101 - GCTGGAGAGGCGTGGAGAGGGGGGCTGGGCGCCGGGGACGTCTGGGTCCCGCGCCCAATG - 2160
2161 - GCTGGAGGGCGGCCGAGCGCCGCCCGCCCGCCCTGCCCGCCCCCTCTCCCCTCCCCCCGG - 2220
2221 - CACTCCCCTCCCCCTCCCCCGCCCGCCGCTTTCCCCCGCCCCCGCCCCGGCGCCAACTCC - 2280
2281 - GCGGCGCCTCCTTAAAAAGCGCGCGGAGTTGTAAGGGGGGGCCGGAGCGAGCCGGAGTG - 2340
2341 - AGCGAGAGCGCAGGGTAAAGGGGGCGGGCGGGGGGCCCGGGCTCCACCTTAAAAGCGGGC - 2400
2401 - GCGTGGGGGTGGGAGGGAGGAAGGCGGGCGGCGGGGAGGAGGGAGGGAGGGAAGGAAGGG - 2460
2461 - GGGCCGGAGTGTCCCGGGCGCAGGGCGCGCGTGCGGCGGCGGCGGCGGCGGGGAGGGGCC - 2520
2521 - GGCCGCGCCGCGCTCCCCTCCTCCCCCTCGCATCCCCGGCCCCGCGCGCGCCCAGCAGAA - 2580
2581 - GCGGGTCTGTGTGTGCGTGCGTGCGAGTGAGTGAGTGTGTGCATATTTTTTTCTCTCTTT - 2640
2641 - TCTTTCTCTCTCACTGTTTTTTCCTCTCTCTCTCTCTCCCTCTCTCTCTCTTTTTTTTTT - 2700
2701 - TTTTTTTTTTGCAAAGAAACAGCAGCGCCGCCGCCGCTCCGCCGAGGCGCTGCGCCCCCC - 2760
2761 - GGGGGGGGAGGCGGAGGAGGCGGGCAGCGGCGGAGGGAGGGGAGCCGGGGAGGGGGGCGC - 2820
```

Fig. 23 (continued; 2/6)

```
2821 - CGCGCTGGGAGGGAGGCAGCGCGCACGGTGCAGCCGGGCCGGGCGGGAGGCATGGCGGGG - 2880
     -                                                       M  A  G

2881 - CCCCCGGCCCTACCCCCGCCGGAGACGGCGGCGGCCGCCACCACGGCGGCCGCCGCCTCG - 2940
     - P  P  A  L  P  P  P  E  T  A  A  A  A  T  T  A  A  A  A  S

2941 - TCGTCCGCCGCTTCCCCGCACTACCAAGAGTGGATCCTGGACACCATCGACTCGCTGCGC - 3000
     - S  S  A  A  S  P  H  Y  Q  E  W  I  L  D  T  I  D  S  L  R

3001 - TCGCGCAAGGCGCGGCCGGACCTGGAGCGCATCTGCCGGATGGTGCGGCGGCGGCACGGC - 3060
     - S  R  K  A  R  P  D  L  E  R  I  C  R  M  V  R  R  R  H  G

3061 - CCGGAGCCGGAGCGCACGCGCGCCGAGCTCGAGAAACTGATCCAGCAGCGCGCCGTGCTC - 3120
     - P  E  P  E  R  T  R  A  E  L  E  K  L  I  Q  Q  R  A  V  L

3121 - CGGGTCAGCTACAAGGGGAGCATCTCGTACCGCAACGCGGCGCGCGTCCAGCCGCCCCCG - 3180
     - R  V  S  Y  K  G  S  I  S  Y  R  N  A  A  R  V  Q  P  P  R

3181 - CGCGGAGCCACCCCGCCGGCCCCGCCGCGCGCCCCCCGCGGGGCCCCCGCCGCCGCCGCC - 3240
     - R  G  A  T  P  P  A  P  P  R  A  P  R  G  A  P  A  A  A  A

3241 - GCCGCCGCGCCGCCGCCCACGCCCGCCCCGCCGCCACCGCCCGCGCCCGTCGCCGCCGCC - 3300
     - A  A  A  P  P  P  T  P  A  P  P  P  P  P  A  P  V  A  A  A

3301 - GCCCCGGCCCGGGCGCCCCGCGCGGCCGCCGCCGCCGCCACAGCGCCCCCCTCGCCTGGC - 3360
     - A  P  A  R  A  P  R  A  A  A  A  A  A  T  A  P  P  S  P  G

3361 - CCCGCGCAGCCGGGCCCCCGCGCGCAGCGGGCCGCGCCCCTGGCCGCGCCGCCGCCCGCG - 3420
     - P  A  Q  P  G  P  R  A  Q  R  A  A  P  L  A  A  P  P  P  A

3421 - CCAGCCGCTCCCCCGGCGGTGGCGCCCCCGGCCGGCCCGCGCCGCGCCCCCCCGCCCCCC - 3480
     - P  A  A  P  P  A  V  A  P  P  A  G  P  R  R  A  P  P  P  A

3481 - GTCGCCGCCCGGGAGCCGCCGCTGCCGCCGCCGCCACAGCCGCCGGCGCCGCCACAGCAG - 3540
     - V  A  A  R  E  P  P  L  P  P  P  P  Q  P  P  A  P  P  Q  Q

3541 - CAGCAGCCGCCGCCGCCGCAGCCACAGCCGCCGCCGGAGGGGGGCGCGGTGCGGGCCGGC - 3600
     - Q  Q  P  P  P  P  Q  P  Q  P  P  P  E  G  G  A  V  R  A  G

3601 - GGCGCGGCGCGGCCCGTGAGCCTGCGGGAAGTCGTGCGCTACCTCGGGGGCAGCGGCGGC - 3660
     - G  A  A  R  P  V  S  L  R  E  V  V  R  Y  L  G  G  S  G  G

3661 - GCCGGCGGTCGCCTAACCCGCGGCCGCGTGCAGGGGCTGCTGGAGGAGGAGGCGGCGGCT - 3720
     - A  G  G  R  L  T  R  G  R  V  Q  G  L  L  E  E  E  A  A  A

3721 - CGAGGCCGTCTGGAGCGCACCCGTCTCGGAGCGCTTGCGCTGCCCCGCGGGGACAGGCCC - 3780
     - R  G  R  L  E  R  T  R  L  G  A  L  A  L  P  R  G  D  R  P

3781 - GGACGGGCGCCGCCGGCCGCCAGCGCCCGCCCGTCTCGCAGCAAGGTGAGCGCGCCGGGG - 3840
     - G  R  A  P  P  A  A  S  A  R  P  S  R  S  K

3841 - AGCGGGGGCGCCGCGCGGTGGGCAGGTGCGGGCGAAGTTGGTGGCGGGGGCGCGAGTCCC - 3900
3901 - GGGAGGAACTGGGTGGCGGGTGGCTGGGGCTTTGCGCGCGTTTCCTGCGGGCTCGGTGCG - 3960
```

Fig. 23 (continued; 3/6)

```
3961 - TGGTGACCTTGGCAAGTGATTGAATCTCCCGGAGCCTCAGTTTCCTCCGCTGTAAACGCG - 4020
4021 - GTTTAATAACAGTAGCGACCCCTTGGGGTTGTTGAGCGAGTTTAGTAAGATTTGGTTGTC - 4080
4081 - GAGGGCTTTAGTTAACACAGAGCCTGGCACGGAGTGAATGCGTAAAAGTTAGTCCGTATT - 4140
4141 - GTTCTTAAAGGTGGAATCGGTTCCTCCTCCCCACCGCCCGGACGCCACAGTCAGGGTCTG - 4200

4201 - GGATTAGAACAGCTACTAATTTTGCATGCTTCTCTCCTCGGCTCCAGAGAGGTGGAGAAG - 4260
     -                                                  R  G  G  E  E

4261 - AGCGAGTACTTGAGAAAGAAGAGGAAGAAGATGATGATGAAGATGAAGATGAAGAAGATG - 4320
     -   R  V  L  E  K  E  E  E  E  D  D  D  E  D  E  D  E  E  D  D

4321 - ATGTGTCAGAGGGCTCTGAAGTGCCCGAGAGTGACCGTCCTGCAGGTGCCCAGCACCACC - 4380
     -   V  S  E  G  S  E  V  P  E  S  D  R  P  A  G  A  Q  H  H  Q

4381 - AGCTTAACGGCGAGCGGGGACCTCAGAGTGCCAAGGAGAGGGTCAAGGAGTGGACCCCCT - 4440
     -   L  N  G  E  R  G  P  Q  S  A  K  E  R  V  K  E  W  T  P  C

4441 - GCGGACCGCACCAGGGCCAGGATGAAGGGCGGGGGCCAGCCCCGGGCAGCGGCACCCGCC - 4500
     -   G  P  H  Q  G  Q  D  E  G  R  G  P  A  P  G  S  G  T  R  Q

   1 - AGGTGTTCTCCATGGCAGCCATGAACAAGGAAGGGGGAACAGGTAAGGATCCCTCTGGGT - 60
     -   V  F  S  M  A  A  M  N  K  E  G  G  T

  61 - GGGGAAGAGTGCTAGGTGGAGAGGAACTCAGCCCGAAGACAAAGCCAAAGACAGGTGTTT - 120

 121 - TTTTCCTTCCCAGCTTCTGTTGCCACCGGGCCAGACTCCCCGTCCCCCGTGCCTTTGCCC - 180
     -               A  S  V  A  T  G  P  D  S  P  S  P  V  P  L  P

 181 - CCAGGCAAACCAGCCCTACCTGGGGCCGACGGGACCCCCTTTGGCTGTCCGTAAGTTGGG - 240
     - P  G  K  P  A  L  P  G  A  D  G  T  P  F  G  C  P

 241 - GTATTGGAGACATGGGGGTGCTGCTCAGGTGTGTGGTACAGCCAGAGAGACATCCGTGTT - 300

 301 - CACTGGTGTCTGTTTGTTTTGATGCAGTCCCGGGCGCAAAGAGAAGCCATCTGATCCCGT - 360
     -                              P  G  R  K  E  K  P  S  D  P  V

 361 - CGAGTGGACCGTGATGGATGTCGTCGAATATTTTACTGAGGCTGGATTCCCGGAGCAGGC - 420
     -  E  W  T  V  M  D  V  V  E  Y  F  T  E  A  G  F  P  E  Q  A

 421 - GACAGCTTTCCAAGAGCAGGTGAGTTTCCAGCCCAGGACTACACACTGACAGACACAGAG - 480
     -  T  A  F  Q  E  Q

 481 - GGCCTCCCTGGGATGTGCCCTGATCCCGGCTTTCTCTGTTCCTGTCCCACCCAGGAAATT - 540
     -                                                        E  I

 541 - GATGGCAAATCTTTGCTGCTCATGCAGCGCACAGATGTGCTCACCGGCCTGTCCATCCGC - 600
     - D  G  K  S  L  L  L  M  Q  R  T  D  V  L  T  G  L  S  I  R

 601 - CTCGGGCCAGCCCTGAAAATCTACGAGCACCACATCAAGGTGCTTCAGCAAGGCCACTTT - 660
     - L  G  P  A  L  K  I  Y  E  H  H  I  K  V  L  Q  Q  G  H  F
```

Fig. 23 (continued; 4/6)

```
 661 - GAGGATGATGACCCCGATGGCTTCTTAGGCTGAGCGCCCAGCCTCACCCCTGCCCCAGCC - 720
     - E  D  D  D  P  D  G  F  L  G  *

 721 - CATTCCGGCCCCCATCTCACCCAAGATCCCCCAGAGTCCAGGAGCTGGACGGGGACACCC - 780
 781 - TCAGCCCTCATAACAGATTCCAAGGAGAGGGCACCCTCTTGTCCTTATCTTTGCCCCTTG - 840
 841 - TGTCTGTCTCACACACATCTGCTCCTCAGCACGTCGGTGTGGGGAGGGGATTGCTCCTTA - 900
 901 - AACCCCAGGTGGCTGACCCTCCCCACCCAGTCCAGGACATTTTAGGAAAAAAAAAATGAA - 960
 961 - ATGTGGGGGGCTTCTCATCTCCCCAAGATCCTCTTCCGTTCAGCCAGATGTTTCCTGTAT - 1020
1021 - AAATGTTTGGATCTGCCTGTTTATTTTGGTGGGTGGTCTTTCCTCCCTCCCCTACCACCC - 1080
1081 - ATGCCCCCCTTCTCAGTCTGCCCCTGGCCTCCAGCCCCTAGGGGACTAGCTGGGTTGGGG - 1140
1141 - TTCCTCGGGCCTTTTCTCTCCTCCCTTTTTCTTTCTGTTGATTGTCGCTCCAGCTGGCTG - 1200
1201 - TATTGCTTTTTAATATTGCACCGAAGGTTTTTTAAATAAAATTTTAAAAAAAGAAAAAGG - 1260
1261 - GAAAAAAAAGCCACGGAGTCCATTTTATGAATGGGGTGGGGAGAGGGCACTAAAGAGCCT - 1320
1321 - CCTAAGAGAGCCTCAGGTTAGGACAGAATTGTTTGGGGAGGGAGAAAAACAGAAACAATG - 1380
1381 - AATTATAGCTGCCTCACAGCCATGTATAACAATAATTGCTCCAGGAAGGTGGGAATATTT - 1440
1441 - GCTTTTTTTTCTTCTGTAATCTCACCGTGTCCGTGTCCAGAACAGAGCTAGGCACACAGC - 1500
1501 - AGGTGCTCAATTTTTGTTTTTCGTTTAGACAGGTTTCATTCTTTCACCCAGGCTGGAGTG - 1560
1561 - CAGTGGTGCTATCATAGCTCATTGTAGCCTCAAACTCCTGGGCTGAAGTGATCCTCCCAC - 1620
1621 - CTCAGCCTCCTGAGTAGCTGGGACTACAGGTGCACTCTGCCATGCCGGGCTAACTTTTAA - 1680
1681 - AAATTTTTGTCCGGGCACAGTGGCTCATGCCTGTAATCCCAGCACTTTGGGAGGCCGAGG - 1740
1741 - TGGGTGGATCATGAGGTCAGGAGTTCAAGATCAGCCTGGCCAAGATGATGAAACCCTGTC - 1800
1801 - TCTACTAAAAATATAAAAAAAAATTAGCTGGGCGTGGTGGTGGGTGCCTGTAATCCTAGC - 1860
1861 - TATTCAGGAGGCTGAGGCAGAGGATTGCTTACACCTGGGAGGCGGAGGGTGCAGTGAGCC - 1920
1921 - AAGATCGTGCCACTGCACTCCAGCCTGGGTGACAAAGTGAGACTCTGTCTCAAAAAAAAA - 1980
1981 - TCTTTGTGTGTGTGTGGAGATGAGGGTATGCACTTTGTTGGCCAGGTTGGCCTCGAACTC - 2040
2041 - CCAGCCAAGCAATTCTGCCTGGGATTACAAGCGTGAGCCACCATGCCTGGCCTCAAATAT - 2100
2101 - TGTTGAATGGCTAGCAGTTAAGTCCTTGGGTTTATAAGCATTTCCTCAACTGTCCTCCCA - 2160
2161 - AGTCCCCATAAGACAAAAAACTCATAAAATCCCACCTTACAGAAGAGGCAGCTGGCCCGG - 2220
2221 - CACAGAGATGCTGTCTGCCCCGGGTCACACAGGGTGGCATCTGACACCCTGTCTGAGTTC - 2280
2281 - TTCACTCAGAGTCTTTAAATATAATTAGCGTATTTGACATAATGTACATTAAAAACTATA - 2340
2341 - AACCTGTCAGCCTTTGTCTACTGCAAAGAATCCACTACAAATATTGGGGCAGGGATCTGT - 2400
2401 - TCTTGGACCATAGTAGTGTCTCCAGACCTCATGGTCCTCTTCATTAAAACAACAGAAAAT - 2460
2461 - TCCTTCTGGGCCATCAGATGAGACCATGAGATAGAAGATTTCCAAGTGAAGATTTTGTTT - 2520
2521 - CAAGACAGAGTCTTGCTCTGTCACTCAGGCTAGAGTGTACTGGTGCAATCATAACTGTGG - 2580
2581 - TGACAGCCTCGAACTTTTGGGTACAAGTGATTCTCATGCCTCAGACAACACCCAACTAAT - 2640
2641 - ATTTTGGTTTTTGTATAGACAGGGTCTTGCTATGTGGCTTAGGCTGGTCTTGAACTCCTG - 2700
2701 - GCCTCAAGCAGTCCTCCCGCTTCAGCCTCCTAAAGTGTCAGGATTACAGACATGAGCCAC - 2760
2761 - CAAGTCCAGCCTGAAGATTTTTAAAAATTATTGTTAGTAGTAGTCGCCAGAGTTACTACA - 2820
2821 - TCCAAAGTCCCTACTAAGTTCTAAGTAGTCCCTACTAAGTTCTAAGGCAGTTTCTCAACT - 2880
2881 - CATTAGAGTTGTTTTTTGTTTTTAAAGAAAAAAAGAGGCTGGGCACTTTAGGAGACCGAC - 2940
2941 - ACGGGAGGATCGCTTGAGTCCAGGAGTTTGAGACCAACCTGGGCAACATGGGCCCCCATC - 3000
3001 - TCTAAAAATTTTAAATTAAAAAAATGTTTTAACAACAAAAAGCGTTCTGGGAGTGAGGGG - 3060
3061 - CTGGGGCCTGGGCGGCCTCATTCCATATACCTGTGCCGGGTTGAGGGGTTGGAGACACGT - 3120
3121 - TTAGAGACCCCTCCACTCTAGGAATCCACCTCGAGAGATAAAGGTCCCGGCCCTAGCCAC - 3180
3181 - ACCCCCAGGACACGGCCAGAGGCCACCTCCCTAGGCGGGTCCCTCCCCACCGCCAGGTTC - 3240
3241 - CTGGAGCGCGTGCGGCGCGTGTGCAGGGGTAGGGGGCCGCAGGCGCGCGGACTGGAGAGG - 3300
3301 - CGCGCCCCTCCCGCGTGTTGAAATTCAAAAGAGGCGAACGGCCCCCGGCGCGGCGGCGCG - 3360
3361 - GCTCCGGTGGAGAGGTCAAGGCAGGGGCCAGTCGGAGGCTCCCGGGGCGGGGTCGAACCC - 3420
3421 - GCGGCCAACCTGAGCAGCAGCGGAAGCTTAAAGAGCTCAGGTTCCCGCCCCCCGGCCCTA - 3480
3481 - CCATGGCTACAGAGCAGTGGTTCGAGGGGTCGCTCCCCCTGGACCCTGGAGAAACACCGC - 3540
3541 - CTCCAGACGCCTTGGAACCTGGGACGCCGCCCTGCGGAGACCCCTCCAGGTCGACGCCCC - 3600
3601 - CTGGCAGGCCTGGGAACCCATCTGAGCCGGATCCTGAAGATGCCGAGGGGCGGCTGGCTG - 3660
3661 - AGGCCCGGGCCTCCACGTCTTCCCCCAAACCTCTGGTCCCCCGGCCTGGGCCAGCACCTC - 3720
```

Fig. 23 (continued; 5/6)

```
3721 - CCCGCCTATCCCTGGACACTTTGTTCAGCCCCATCACCCAACAGCTGCGCTACCTACTGA - 3780
3781 - AGAAGGCAGATGATTTCCAGAGCTACTTGCTCTACAGGTGATGCTGGACAGGGTCCCAGG - 3840
3841 - TCCCCATGGGTAAGGAGACTTGGAGGGGAGGCGACAGGATGGGTGACACACACCAGGGTC - 3900
3901 - GCAAAATTACAAGCGCTAGGAGCCAGAGGGAGACAGTGGAAGAAGCTAGCATATTAGAAT - 3960
3961 - CCAGTTTAAGAGAATGAGGAAGACTGTAGAATTGCGGGTAGGGGATGGCTGCTATTACTG - 4020
4021 - TCGTGGCAGGGTGGGCCTGGGGTTGTCAAGTCTCTAGGACTTTTTCTCCCAGTTTTTAAG - 4080
4081 - TGCTGTCTTACATTTTGAGCCCTGTGCTGGCTAAACAAGACCCACCTGAGCCAAACTTGG - 4140
4141 - CCTGCAGGACATCAGTTTGAGACTCCAAAGGATAATGTGATTCCCAGACCAGGTTTCCCT - 4200
4201 - GTGACTCTCAATTTCAGTGTCCATTGGAATTTCCTAGGAGGCTGGGTTGGGTTTGTTTGC - 4260
4261 - GTGTTTGTTTTTGAGATGGAGTCTCACTCTGTCGCCCAGGCTGGAGTGCAGTGGTGCAAT - 4320
4321 - CTCAGCTCACTGCAACCTCCGCCTCCCGGATTGAAGCAATTCTCTGCCTCAGCCTCCCGA - 4380
4381 - GTAGCTGGGATTACAGGCGCCCACCAACATGTGTTGCCCGGCTAATTTTTTTCTTTTCTT - 4440
4441 - AGTAGAGACAGAGTTTCACCATCTTGGCCAGACTGGTCTTGAGCTCCTGACCTCATGATC - 4500
4501 - CACCCGCCTTGGCCTCCCAAAGTGCTGGAATTACAGACGTGAGCCACCGCGCCTACCCGA - 4560
4561 - GGCTGGGTTTTTTTGTTTTGTTTTGTTGTTATGTGTTTTTTTGAAATGGAGTCTTGCTCT - 4620
4621 - GTCACCTAGGCTGGAGTGCAGTGGGGCGAACTCAGCTCACTGCAACCTCCGCCTCCCAGG - 4680
4681 - TTCGAGGGATTCTCATGAGGCTGTTTTTTTTTTTTTTAATGAGACAGGGTCTCGCTCTGTC - 4740
4741 - ACCCAAGCTGGAGTGCAAGTGGGGCAGTCATAGCTCACTGCACCCTCGAACTCCTGGTCT - 4800
4801 - CAAGCAATCTTCCACCTCCCCTCCTGGGTAACTGGGACTACAGGTGCCACCATGCCCAGC - 4860
4861 - TAATTATTTTTGTGTAGAGATGGGTTCTTGCTATGTTGCCTAGGCTTGTCTGGAACTCCT - 4920
4921 - GGCCTCAAGCAATCCTCCAGCCTCAGCCTCCCAAAACTCTAGGATTGCAGGCGTGAGCCA - 4980
4981 - CTGTGCCCAGACCCTGCAGGAAGCTCTGGGTCCTAAGTGTTGTGACACTCAGGTGTCAGC - 5040
5041 - ACTTTAACAAGTGTTCCAAATGGGTTTGATGCAGGTAAACCAGAAAGATGTTCAGAAAAG - 5100
5101 - ACCTGAAACTGGGGGCTTTTCTAATGGGTCAAAGCCAGGGATACAGGTTGGGATTGAGTA - 5160
5161 - GAATGGGGAAAACTGCGGGGTGGGGAGGGGTTGTGAGGGATTCCAGGCAAAGGCCCCCTT - 5220
5221 - CTTCCTTCAGCAGAGACCAAGTACAGAAGGAGCAGCTGGCCAAGGCCATGCCCACCTTCT - 5280
5281 - TACAGATGTGTGAGCCCTACTTCCTGTACCTGGAGGCAGCCGCGAGAAGCATACCCCCCA - 5340
5341 - TCTATGGACCCCTGCAGGAGCTGGTCCGAAAGGGGGTGTGTGGAGGTTTCTTAGACCCCA - 5400
5401 - CGCCCCTTTCTTCTCGCAGCTCTGAGCCTGTGGGGATGGTGGAGGGGGAGGCCCACTCCT - 5460
5461 - CGCAGGCCAGCTGATCTCACTGTACCCCCCTCTTGTATGCAGCTGTTAGAGATCTCCCAA - 5520
5521 - CAGCTGACCCTGCGCCTGGAACAGCTGGTCCTCATGTACGCTTCCTTTGGGTTCGTGGAC - 5580
5581 - CTGGAGGAGATGAACCCCCTTAGGTAAAATGGTAGGAGACTCAGATGGGGGGATGAAGGA - 5640
5641 - GTCCAAGGCCCAGCCTCACCCCTCCATTCTCTCATGTCTCGCCAGCATCTCCTGTTTCTT - 5700
5701 - TTGCGGGAGGTTCTCCATCAGCCTGTCCCATGAGGTCTCCATCTTCAGATACTGTGCCCC - 5760
5761 - AACCGCCTACACTGCCAGCCGCTTCCCCCGCTACCTCTATAAGAAGATGCGCTGGCACCT - 5820
5821 - GGAAGCCACCCCAGAGGCCCCTGGTCGGGGACAAGATTCCCTTGTGGATTAGTAAGTCCT - 5880
5881 - CTTACCCAAATCAAAGTCCTCCCCTTTCTATGATGAATGCCAATATGACCCTCCAAACCG - 5940
5941 - TCACCAGCAAAGTGAAAAGTGAGCCAGGGCCCGAGGCAGTGGCTCACGCCTGTAATCCCA - 6000
6001 - ACACTTTGGGAGGCCGAGGCAGGAGGATCACTTGAGCTCAAGAGTTTGAGATCAGCCTGG - 6060
6061 - GCAAGATGGCAAGACCCTGTCTCAACAACAAAGAAATTCGCCAGGCGTGATGGCTGGCAC - 6120
6121 - CTGTAGTCCCAGCTACTTGGGAGGCTTAGGCAGGAGGAGCACTTGAGCCCAGGAATCAAG - 6180
6181 - GCTACGGTGAGCTGTGATTGTGCCACTGCACTCCACCCTGAGTGGAAGCAATAATCTGTC - 6240
6241 - TCTTAAAAAAAAAAAAAAGTGAACCAGGAAACTAAAGGCTTTTGAAAGGCTACCTCTATT - 6300
6301 - TTCTTAAAACCCACCCTCCCACCAAAATAAAAGTTCTCATCTTAAAAGTAGGCTGGCAGG - 6360
6361 - GAGAAAAGGCCTTGGAGTCACATTCCTACCTGAGAACTTCAGGGCAACTTCTGATGAGTT - 6420
6421 - CCCACCTCAACTCCAAAATTAAAGCCCTCAACAGAAGTAGCTAGGAAGCTGATCACTTCT - 6480
6481 - AATTACAGCTCCCTCCCCTCCTAGCTACTTTCTGTGCTATCGAGATACTTGGGAAGACAC - 6540
6541 - AGGCCAGAGTCCAGCCAATTCGTGCCCACAGATCCAGAAGCTGTGGTCCATCGGCCGATG - 6600
6601 - GGTGCCCCTAGGACCAGCCGAGGATGACCTTTATTCATGGTAGGAGCTAGGGCAATAGCA - 6660
6661 - ACGTGGGCCTGGGAGCTGGAGGGGGAGGCAGAACCCCACCAAAGACAATCCACCTTCCCA - 6720
6721 - AACACTTTGCTTCCCTTAGTAGTGATAGCATTTTATTGTGCCCTGAAAAGCACTTCATGC - 6780
6781 - AGACCCCAGTAACAACCCATGGAGATCTATGCTATTGGCCCCATTTAACAAAGAAAACAG - 6840
6841 - GGTGCTCAGAGAAGTTGTTACCTGCCCAAGGACACACAGCTAGCAGAGCGAATGGACAGG - 6900
6901 - TCAGGACCAGTTATTCAGCCTCTAGGAGCCATTACTAAGTCTCTGATCAACAAGGAAACA - 6960
6961 - AGTTTCCCCCGGGGGTTTTTCCCACCCGCAGCTGAAACAAAGCCTCTTTCACCTGAGCCT - 7020
```

Fig. 23 (continued; 6/6)

7021 - CTCACTCAAAGGGAGGGACTCCCGAGGGGCAGGGGGCACTCAAGTCCAGGCCTGTCTATC - 7080
7081 - CCTGGCCCCCCCACCCCAGGATTTTGTGCCCGCACCGCTTGGGGACTACCAGCAGCTGCT - 7140
7141 - GACCATCGGCTTCGAGGAGCCCACGCCCACGCTGGCCACCGACCTGCTGGTGCAGATCCT - 7200
7201 - CACGGGCCAGGCAGGCCAGGCCCGGCCTCCGAGCGCAGCCGGGCCTGCGGGGTGGGCAGC - 7260
7261 - GCAGGGGTCTTGAACCTGGGGAAGAGGGTAGGAGCTGGAACTTGACAGTTCCAAACTCCA - 7320
7321 - GAATAGGGGGCAGGGGAGGGGCTCACTCGTTCTCGCAGTGCAGCCGGGCCTCGCCTTCCA - 7380
7381 - AAGGGCCAGGCCGAGCTGACCTGTCTGCACCGAGTCCGGCTTGGCCGTGGGGCCCTGAAT - 7440
7441 - GCGGACACGTCAGTTTTGTGTTAAATAAAAGAAAGAAAGAGGTCACAGGCTCAGCGTCCG - 7500
7501 - CTGCGAATGCCGCGCCCCTCCCCCGGGGGATTGCCCCACCCACTCGCGTGGCCTTCTGGG - 7560
7561 - AAATGTAGTCTTTTGAAAGAAGCCTGGAATTCGCCAATAGGCGGACGAGAGTTTGGCGCA - 7620
7621 - TGCGCATAGGCGCACATGAAGCAAAAAGGGAAGTGGTGCCCGTCAACACCGGAACCCAGA - 7680
7681 - AAACTGCAAGTTTAGGGTACCGGGGAAATTCAACGTCCACTGGAGGAAGAGACTTAAGGC - 7740
7741 - TACGCCCACTCCCATATTTTGACCCGGAAGTTATTTATTTTAGCGTAGAAGACTACTTTT - 7800
7801 - CCCGACGCGCCCCAGGAAAGTGCCCTCGATCAGTTTCCTAAGGGCCCGAGTTAGACTTTT - 7860
7861 - TTTTTCTCTTCCAGCTTTTGGGACTTGGGGGCCGGACAGGTCGTCGTCTTTCTTGGGGTA - 7920
7921 - TCCGGGGTGCGGACAAGGTGGGAGAGCCCTACGGTATCCAAGCTT - 7965

Fig. 24 (1/9)

```
   1 - CAACATGCTTGGGACCAGAAGTGTTTCCAATTTGGGATTTTCTCAAATTTTACCGGTTGA - 60
  61 - GCTTCCCCAATCTGAAAATCTGAAATCCAACATGCACGGCTCTGAAGTCTTTCACTGAGC - 120
 121 - CTTTGGGGGAAATATTTAACATCCTAACAGCCCTAAACCAACGCTCAATTAGCACAACAG - 180
 181 - TTTACAATCTTCTCTACCCACAGCCTGATGCGAGGCTCTGGGACTAGACTATTTAGCCAA - 240
 241 - CAGTTCTTGCAAAATTAACTGACTTATAAGTAAATAGTAATTTCAACACCTCACTGCTAA - 300
 301 - TGCTGTAACAACTCTGCAGACCTAGGGAGCAAGTACGGTTTGCAGAGCACTGGGAAGGCT - 360
 361 - CTGAAGTGACCTTTGAACTGGGCCTCAAAAAATTTTGGGTTTGGCAAAAGTCAAATCTCT - 420
 421 - TAGGCTTCAAATTCCAGGCACAAGGATTGTTGGGTTTGATTTCATTATCCAGAAGCAATG - 480
 481 - GGGATACAGAATTGTGATCTCATGTGTAGGGAACTGTGGGGGTTTTTTCTACTTTAACCC - 540
 541 - CAGTGAGACTTTGTAGAGTGTGGGGTAGAGAAAAGGCTCATGAATATGCCTGAAGCCTAA - 600
 601 - CTCAGCACCTTTCTGAGGAACTGACTGCCAAAATGGTAATGGAGAGGGGAAAATATGACC - 660
 661 - TACTTTCACAAGTTACCTTGACTGCCTCAGGGAAACCTGCTGTGGTAGTGTTTCTTCTGG - 720
 721 - GTGAAAGACCAGGTAATTACCTGGGTGCTGGTCTCAGACTTACCAGTTTTGAATCCCTGT - 780
 781 - TTTAACCACTCACTATCGATATGACCTTGGATAAGTTACCTAACCTTTCTCTTACTGTCC - 840
 841 - TTTTCCGTAAAATGGGGATAACAGATAGTAGTTATTTCTATGAGTGGTTATGAGAACCAA - 900
 901 - GCTATTAGATAGCGGGAAAGCACACAGTAAGCGTTCAAGGAACTGCTATTGTTATTAAAA - 960
 961 - GCCTCCTTTGGAAGAAGGACATTGAGGCCCAGAGAGAGAACAGAACGTCCAGCCACACAG - 1020
1021 - CAAATCCGTGATGAAGTTGGGACTGGAGTATGGGTCTCCTGAGTCTCAGCCCAGGACTCT - 1080
1081 - ATCCCTCTTCCCGAGTCCTCGGAGTTCCCGGATGGAGTCACATTTGTTCACGGCCAGGGA - 1140
1141 - GGAAGGTTTGATGGAGGCCTGCAGGAAACAACAGCCAGGCGCAAGGCTTTGGGAGTTGAA - 1200
1201 - GCATAGCTTCTGCGAGATAGAAACAAGGTTGACATGGGCACTCGTGCAGAATGACGGGCT - 1260
1261 - CCTTTTGGACTCCCAGGACTACAGTCCCTTATGCACCTTGGGATCTGCGGCTAGCCCCTG - 1320
1321 - CGTAAAGAGGGACGCGTAGTCTTTTCCCTGCCCCGCCCTGCCGGGGCGCCCGCCTCCGAG - 1380
1381 - GCCGCCCTCGCTTCGTCCTTCCCAGCAAGCTCCGCGCCGGCGCCGGCTATTGATTGGCTG - 1440
1441 - AGGCGGGAGCAGGCGGCTGGCCGGCAGCAGTTACTCGGGGTTTCCGGTGCGAGGCCAGAG - 1500
1501 - GTGGGGAAGCCATCGGACGTCGGCGGTGAGGTACGTGCAGCGGCGGCCGGTGGGCGAGAC - 1560
1561 - TATTTGAGAGTGTGCGGGCCGGGATGTTCTCGGCCTGTGGGGAAATCACGCCAACTCCCC - 1620
1621 - GCGTGGGCCGGGGGCTGTCTGGGGATATGCGCATGCGCGGGCGTGCCTCGCGGCTTGAGG - 1680
1681 - GCGCGCGGGGCGTGGGTGGCTGCGCGCGCGGGGGGCGCACGTGGGGCCTGAGGGGCGGGG - 1740
1741 - GCGGTGCCGGGAGTCCCGCCACGTCAGTCTCCGGCCCTGAGCCAATCCCGCGCCCGGCCT - 1800
1801 - GCCGCGAGGGGGCCGGTTGTGCCGGGAAGTGGCTCCAGGGAGAAGAGGCCTCTTCCCTCA - 1860
1861 - CCCGCTGTGGGAGCTGCGCCCCGAAAGCCTGCCCCGGCACGTCGGGCTCTCCTGACCCGC - 1920
1921 - CAAGACCAGAGAGCCGTTGGCGCCCTCCGCCCGGGCCTGCCGGTCCGTTTATTTTAAGAA - 1980
1981 - GCTTTGTGCGCCTGCTGTGGGGATTTCTGATCCAGGCTGCGAAGAATTTCGAAGTCTGGA - 2040

2041 - AAATAGCAACTGTGTTTGTTTCTAAAGGATCTTCTCCTGACCCAGCATCGCTCATCACAA - 2100
     -                                                          M

2101 - TGAAGAACCAAGACAAAAAGAACGGGGCTGCCAAACAATCCAATCCAAAAAGCAGCCCAG - 2160
     -   K  N  Q  D  K  K  N  G  A  A  K  Q  S  N  P  K  S  S  P  G

2161 - GACAACCGGAAGCAGGACCCGAGGGAGCCCAGGAGCGGCCCAGCCAGGCGGCTCCTGCAG - 2220
     -   Q  P  E  A  G  P  E  G  A  Q  E  R  P  S  Q  A  A  P  A  V

2221 - TAGAAGCAGAAGGTCCCGGCAGCAGCCAGGCTCCTCGGAAGCCGGAGGGTGTGTGCCAGC - 2280
     -   E  A  E  G  P  G  S  S  Q  A  P  R  K  P  E  G

2281 - TCTGCGTTGCCAGCGGGCAGGGGGAGGAGCTGTGGGGTCGGCCTCGCTTCTGGACTTACA - 2340
2341 - GGCCGAGGCCAGGTTGTCCGGGAGGAGGAGATGTAGAATGAGAGGACAGTGCTGGGGGCC - 2400
2401 - GCGGTCCCCCCTGCGCTCTGGCGAGTTGGCGGAGCTGCCCCCTCTAAGCACAGGAACAGA - 2460
2461 - GTTCTGGAGAGAAGCTCCGACGGGATTAAGTCAGGTGGCAGCCAAACGAGGCACCCAGTC - 2520
```

Fig. 24 (continued; 2/9)

```
2521 - AGGAAATCCAGGTCCCGTTAGAAACACCTCAGCCACCAGCAGCTAACTGCCCTTCCTGTT - 2580
2581 - TGAGGCATTTCTAGAATGATCTGAATGGCAAGAAATGGGTTTTGTGGGGGGGAAGGAGAT - 2640
2641 - GGACTAGAAGTTGCTCCGTGCCATCCCTGTGTGCTGATGCTTTACATACTTTTATGATCT - 2700
2701 - AACAAATATGTTCGGGTGGTAGTGAGAAATAGTTGTGTCATTTTACAAGTAAACAGACTT - 2760
2761 - AAAGAAGTTAGGCAACGATTACTATAATTTCTTGATTTAAAAGATGTTTCGAATCTAAAT - 2820
2821 - TCTGACAGGAACTAGATTTGCTGAATGATACTCCATTCTTGCTTCTCAGTTTCCATAAAA - 2880
2881 - AAAAAAGTTAGGCAACATTTAACTCAAACTGATGAGTTTGGCTGGGCCTGAAAAATCCCA - 2940

2941 - ACCAGTGGTATAATCGTCTTCTTTCTCACTCTACCCCTCATCCTCTCCTGCTGTAGGGGC - 3000
     -                                                          A

3001 - TCAAGCCAGAACGGCTCAGTCTGGGGCCCTTCGTGATGTCTCTGAGGAGCTGAGCCGCCA - 3060
     - Q A R T A Q S G A L R D V S E E L S R Q

3061 - ACTGGAAGACATACTGAGCACATACTGTGTGGACAATAACCAGGGGGGCCCCGGCGAGGA - 3120
     - L E D I L S T Y C V D N N Q G G P G E D

3121 - TGGGGCACAGGGTGAGCCGGCTGAACCCGAAGATGCAGAGAAGTCCCGGACCTATGTGGC - 3180
     - G A Q G E P A E P E D A E K S R T Y V A

3181 - AAGGAATGGGGAGCCTGAACCAACTCCAGTAGTCAATGGAGAGAAGGAACCCTCCAAGGG - 3240
     - R N G E P E P T P V V N G E K E P S K G

3241 - GGATCCAAACACAGAAGAGATCCGGCAGAGTGACGAGGTCGGAGACCGAGACCATCGAAG - 3300
     - D P N T E E I R Q S D E V G D R D H R R

3301 - GCCACAGGAGAAGAAAAAAGCCAAGGGTTTGGGTGAGCAGAGGGCGGCTCTTTGTGAAGC - 3360
     - P Q E K K K A K G L G

3361 - TGGTGAGGAGAGGGAGTTTGGACTTGACGTTCTCTGGGCCAGTCTGTTCTGCCAGGATTC - 3420
3421 - AAAGGAAAACGGTACTTCTCAGAGCAGCAAGTCACTCTAGTCTAATCAAAGCCAGGGATG - 3480
3481 - TGGGGGCCACGGCATAGAGAGATGCAGGAGTTACCAGCACAAAGCCTTCTGGGTTTTGGA - 3540
3541 - GCAACTGGAGCTTGGCATGGGACCTGTTCTCTCTTTGAGAAAATGGAGACGGGAGGCTAG - 3600
3601 - GGTAGGCTCCTGTGCCAGCCAGTACTACCTGCTGTGTGACCTTGGGTGTGTCCCTTCTCC - 3660
3661 - TCTCTGGGTCTTAGTTTATATTTCTCTTTACAGTAAGAAAATTAGACTAGGCCAGAGTTG - 3720
3721 - AAAACCCAAATATCTGCATAAGCTGGGCTTGGCCATGGGGCCACCTGAAGATGGAGGCTT - 3780
3781 - TACTGCTTCCCTGATTAGTTGCTCTCACTAGCCAACTGAGAGCAGGCAAAACTACAGGCT - 3840
3841 - GGGTGCAGTCAGGCTTTTTTTTTTTTTTTTTTTTTTTAAATAAAGAAAAGCCAGAAATCT - 3900
3901 - AGAGTTATGTGAGAACTCTAGATTTTTTCATAGTTAGCAGCTAAAATGGTAAGAGCCAAA - 3960
3961 - CAAAACCCATCCGTGGGTTGGATTTGGCACACATGCCTGCGAATTGCAGTCTCCATGCTG - 4020
4021 - ATCTCTTGGGCCCTTCTGGGGAGGCAGAGGGAAGGCTCCCTGACTCAGTCACAGGCAATG - 4080
4081 - GGGAATAGGCAGTGACAGTCATTTTACAGCAGGGTATGTATGTTTAAGAGTCTAGGCCGG - 4140
4141 - GGTGTGGTGGCTCACGCCTGTAATTGCAGCACTTTGGGAGGCCGAGGCGGGTGGATCACC - 4200
4201 - TGAGGGTCAGGAGTTCGAGAACAGCCTGGCCAACATGATGAAATCCCGTCTCTACTAAAA - 4260
4261 - ATACAAAAATTAGCTGGACATGCTGGCACACGCCTGTAATCCCAGCTACTTGGGAGGCTG - 4320
4321 - AGGCAGGAGAATGGCTTGAACCCGGGAGGCAGAGGTTGCAGTGAACTGAGATTGTGCCAC - 4380
4381 - TACATCCAGCCTGGGTGACAAGAGTGAAACTCTGTCTCAAAAAAAAAAAAAAAGAATCTA - 4440
4441 - GAATCTAAGTCGAGTGTCATTATATCCATGTTTTATTCCTATTCCCTTTTCCCCTTATGT - 4500
4501 - ATCCTCTTACTTTAAAGAGGAACTTTAAAAAATCTTAGGGACGACTAGGCAGAGTGGCTC - 4560
4561 - ACACCTGTAACTCCAGCACTTTGGGAGGCCAAGGCAGGCAGATTATGAGGTCAGGAGTTC - 4620
4621 - GAGACCAGCCTGGCCAACATGGTGAAACCCCAGTTCTACTAAAGATACAAAAAATCAGCC - 4680
4681 - GGGCGTGGTGGCACGTGCCTATAATCCCAGATACTCGGGAGGCTGAGGCAGGAGAATCAC - 4740
4741 - TTGAACCCGTGAGGCAAAGTTTTCAGTGAGCTGAGATCATGCCATTGCACTCCACCTGGG - 4800
```

Fig. 24 (continued; 3/9)

4801 - TGACAGGGTGAGACTCCATCTCAAAAAAAGAAAAAGGAAAAAATCTTAACGTCACATACA - 4860
4861 - TGGAAAGATCATCTTTTTCACCCCCCACCCCCAACTGAGATGGAGTTTTGCTCTTGTCAC - 4920
4921 - CCAAGCTGGAGTGCACTGGCGCGATCTAGCTCCCTGCAAGCTCCGCCTCCCGGGTTCACA - 4980
4981 - CCATTCTCCCTGCCTCAGCCTCCCGAGTAGCTGGGACTACAGGCTCCTGCTACCATGCCC - 5040
5041 - GGCTAATTTTTTTGTATTTTTTTTAGTAGAGACGGGGTTTCATCTGTGTTAGCCAGGATG - 5100
5101 - GTTTTGATCTCCTGACCTCGTGATCCGCCCGCCTCAGCCTCCCAAAGTGCTGGGATTACA - 5160
5161 - GGCGTAAGCCACTGCACCCCGCCTTTTTTTTTTAATTAATTAATTTTTTTAGACAGAGTC - 5220
5221 - TCGCTCTGTCCCAAGCTGGAGTGCAGTGGCGCGATCTGGGCTCACTGCAACCTCCGCCTC - 5280
5281 - CTGGGTTCACGGCGATTCTCCTGCCTCAGCCTCCCGAGTAGCTGGGACTACAGGCTCCTG - 5340
5341 - CTACCATGCCCGGCTAATTTTTTTGTATTTTTTTTAGTAGAGACGGGGTTTCACTGTGTT - 5400
5401 - AGCCAGGATGGTTTTGATCTCCTGACCTCGTGATCCGCCCGCCTCAGCCTCCCAAAGTCC - 5460
5461 - GCCTCAGCCTCCCAAAGTGCTGGGATTACAGGCGTAAGCCACTGTACCCTGCCTTTTTTT - 5520
5521 - TTTAATTAATTAATTTTTTTAGACAGAGTCTCGCTCTGTCACCAAGCTGGAGTGCAGTGG - 5580
5581 - CGCGATTTGGGCTCACTGCAACCTCCGCTTCTTGGGTTCAAGCGATTTTCCTACCTCAGC - 5640
5641 - CTCCGGAGTAACTGGGACTACAGGCGCGTGCCACCACACCAAGCTAATTTTTTTGTGTAT - 5700
5701 - GTCTTTAGTAGAGATGGGGTTTCACCATGTTAGGATGGTCTCGATCTCTTGACCTCGTGA - 5760
5761 - TCCGCCTGCCTCGGCCTCCCAAAGTGCTGGGATTACAGGCATGAGCCACCTTGCCTGGCC - 5820
5821 - GAAAGTATCTTCATTTTAAAGTTCACTGTTTGGCTACTCTGTTGACAAGAGTTTAGTATT - 5880
5881 - TCTCAAGGAGGCTAAGATACCTATTCCTTTTTGGATCCTACCTCTATCAGGAGGGTGGGC - 5940
5941 - CTTCCTTGCATTGAAACAGTATGAAAACAGTAGCCCTGAATTCATAAGTGGGACACCTTT - 6000
6001 - CTTCTATTGGTAGAGCAGGCAGTTTTTTTCTCCTGCCAATGGTGCCTACTAAGGAGATTT - 6060
6061 - CACTAGGGTACAGTCGTTCATTTGATAAGCATTTGTTGAGCATATCCTCTGTGATGGTAC - 6120
6121 - TATGGACAGTACTGGGGCTATAGTGAGGGCAGGATTGAGTTGGTCCTTATGGCAAGGAAG - 6180
6181 - GCAGCTAATCAACAAGCAAAATATAAAGTATGATGGGGAGGGCTGTCTTCAGCACTCATG - 6240
6241 - AGTGTGAGCCCAGGCCTGGAGGGGACACCTGGAGAAGAGGGTGCATGTCTTTGCTCCTGT - 6300

6301 - GCTTTTCAGGGAAGGAGATCACGTTGCTGATGCAGACATTGAATACTCTGAGTACCCCAG - 6360
- K E I T L L M Q T L N T L S T P E

6361 - AGGAGAAGCTGGCTGCTCTGTGCAAGAAGTATGCTGAACTGGTCAGTTCCCCCCTCCGCG - 6420
- E K L A A L C K K Y A E L

6421 - GGCACCTTCCCTGCGTTGGGAAAATCAGCATGCCACCTGGTGTAAGGTTGGGGGTGCAGA - 6480
6481 - GTCAAGTAGGTGGCTTAATTCCTGTTCAGCTTTTCTCTGAACTATCTGTTAAATGGGGAA - 6540
6541 - TCACTTCCAGCCAGCCTCTTCAGGGCTGTGCAGCAAGAGGAGAAACTGCATATTCCTTGA - 6600
6601 - AAGAAATTTCTCAAAGAATGATTCCAAGGTGGTAGAGCCCTTGTTCCTGGCCTGAGTCCA - 6660
6661 - AGACACCTTGTGATCTTGATGCTTCTTCCTCAAATACAGATGCATAGAGCCATTATCACA - 6720
6721 - GTTAATAAAACTAACACTAGTCACTTGATACTTTTTCCTTTTACTCCAGAGCAGTCTTCT - 6780
6781 - TGTCACTGCCTCCTCATATTCCCCATGACATTGACTTTTAACAGAAACTAGACTAGCTGT - 6840
6841 - CTTGTAGGATGCCCCCTTCTAGCTTTGTCATCTCTGTGGTATCATTTTACTTCTTTACCT - 6900
6901 - CCTGGTACATGTAAGTGAAGTAGAAGTTAGCTCTAAAGCTTGATCCAATTCAGCTTCAAC - 6960
6961 - TTTTTGACAAGAATTCTTCATAAGTACTTCATGTTCCATCACAATAAATGCAAAGCATGC - 7020
7021 - TCTTCCCACTTTGTTGTAACATTGTTCAGTGGGTTGGGGGTGGGGCAGCCAGATTCTTCC - 7080
7081 - ATCATCAGGTCCCTTGTCAGAATTTGAACTAACAGATTTATCCATTGATGGTCACAGCCT - 7140
7141 - GTGTATGTATGTATGTATGTATGTATGTATGTATTTATTTATTTATTTATTTTTTGAGAC - 7200
7201 - GGGGTCTTGCTCTGTCGCCCAGGCTGGGGTGCAGTGGCACGATCTCGGCTCGCTGCAAGC - 7260
7261 - TCCGCCTTCTGGGTTCATGCCATTCTCCTGCCTCAGCCTCCCGAGTAGCTGGGTCTACAG - 7320
7321 - GCGCCCGCCACCATGCTAGGCTATTTTTTTTTTTTTTTTTTTTTTAGTAGAGACGGGGT - 7380
7381 - TTCACCGTGTTAGCCAGGATGGTCTCGATCTCTTGACCTCGTGATCCGCCCGCCTCGGCC - 7440
7441 - TCCCAAAGTGCTGGGATTACAGGCTTGAGCCACCACGCCTGGCCTATTTATTTATTTATT - 7500
7501 - CAGAGTCAGAGTCTCGCTCTGTCACCAGGCTGGAGTGCAGTGGCGCGATCTCGGCTCATT - 7560
7561 - GCAACCTCCACCTCCCAGGTTCAAGCGAGTCTCCTGCCTCAGCCTCCCGAGTAGCTGGGA - 7620
7621 - TTACAGGTGCATGTCACCATGCCTGGCTAAATTTTGTATGTTTTAGTAGAGACAGAGTTT - 7680

Fig. 24 (continued; 4/9)

```
7681 - CAGTATGTTGGCCAGGATGGTCTTGATCTCTTGGCCTCGTGATCCGCCCGTCTCAGCCTC - 7740
7741 - CCAAAGTGCTGGGATTACAGGTGTGAGCCACTGTGCCTGGCCTCTAAGTATTTATTTTAA - 7800
7801 - AATTAATTCATTCCACACACATTTATTAATATTTTCCTGTAAGGAACTTTACTCATCTTT - 7860
7861 - AAAATGGGGAATGTCATACCTGCCTAATGACATTCTTGTAAGGATTAAATAAAAGGTATA - 7920
7921 - AGGAAGATAAGCACCCTTTTGGAGTGATCCAGCCAGGGGAAAATTGCTGATGCAAGAGAG - 7980
7981 - GAAATGAGTTGCTAGAGTGGTGTTGTGAGTAGAGGAGGGGAGCTGAGGCCTGCCCAAGAA - 8040
8041 - GGGGGCTTGGCTGTGGTAACCACATGGCTAGGTCTGTGTGACTGGAGGAGAGGACGGGGC - 8100
8101 - AGGTGGACTGGTAGATGTGCAGCTTGTGCCCCTGATTCTCTAGTTTCTTCTGTGTTTTGA - 8160
8161 - GATTTGATGAGAACGATGAAATAGTTGTCTGGAAGGAGAGGAGTGTGAATAGCATATGCA - 8220
8221 - TTGTATTGGGATTGCTGGTCTTCCTGAAATTGGTGGCCATGAATTTAAAGTGAGACTCTT - 8280
8281 - CAAGTAGGGTTGTTATAGTACTGGTGTAAAGCAGGAAGGTGCTTTACTAGGGTTGCAGTA - 8340
8341 - CTACTGGGGAAGGGCCAAGAGAGTTGAGGGTGTAAGAAATCCAAGCCAGGTAATGTAGTT - 8400
8401 - ATTTTAAAGGAGAGTGGAAGGATGGTTGAGTCAATGGATTGGAGGTCCTATAGGGTAAGA - 8460
8461 - GACTTTCTGAGGATCACAGATACTGATTGGAATGAGCTAAAAAGATAGGTGATGGTAGTC - 8520
8521 - CTGGACTGGGATGCTGGAAATTGAGATAGTGGGTGTGCTCTCTGGTAGTGACAAATCTAG - 8580
8581 - ATCTGCGCTGTCCAAGATAAATTCGTCTCTAGCTAATTGACATGTGGCCAGTTTGAATTT - 8640
8641 - GAACATGCTATAAATGTAAGATACACATCAGCTTTTGAAGACTTAAGCAAAAACAAAGAA - 8700
8701 - TATAAAACATCTTTTTGTGAGAGAGTGTCTCAGTCACCCAGGCTGGAGTGCAGTGGCGTG - 8760
8761 - ATGTCCTGCTTCCAGGTTCAAACGATTCTCCTGCCTCACAGCCTCCTGGAGTAACTGAGA - 8820
8821 - TTACAGGCGCATGCCACCAAACTGGCTACTTTTTTGTATTTTTTTTTTAGTAGAAACGGT - 8880
8881 - TTCACCATGTTGGCCAGGCTGGTCTTGAACTCCTGACCTCAAGTGATCTGCCTGCCTCAG - 8940
8941 - CCTCCCAAAGTGCTGGGATTACAGGCATGAGCCACCACTCCCGGCCTCACTTTTTTACAT - 9000
9001 - TGATTCCGTGTTGAAATTGTAATGTTTTGGATATTAGGTTAAATACATATATTACTAAAA - 9060
9061 - TTAATTTCACCTGTTTTTTACTTTTTTAGTGCGGCCAGTAGAATATTTTTAATTACTTAT - 9120
9121 - GTGGTTTGCATTATATTTCTGTTGTACAGGCCTGGATAGGGTCATGGGAGGGGAACTGAG - 9180
9181 - CTGGGGAAAGGAGTGGGTTTGTGGAAGAGGTGATGGACTGTGAGGCCAGGGAGTTAGAAG - 9240
9241 - GATTATCTGTTGATACTGAAGTGGCCACAAATGAGAAAAGTAATTGTGTTGGGGAGAGCG - 9300
9301 - CTGATGAACGCAGCGCTAACGTTTTGAAGGAATGCGAGGGAGCGATGGGGGTCTGTCTGT - 9360
9361 - TAATAGGCACAAGGTACGGTAGCAGGTGGTCTCATCCTCGGGCATGAGTGTCCAGCAAGT - 9420
9421 - TGGGGAAATGCAACAGCTTGAAGTGGCTCTAGTGGCCCAGAGTCAGAGCTGGAATAGGAA - 9480
9481 - TTGGCATCTGCTGGCTGTGTGGCCCCTGCTTGCCCTAGTGAGTTACCATTTCTCTGTCCC - 9540
9541 - TACGGTGGAGCCTTTGGGGTTATTGTGAGTTCATGGGAGGAGCGTGTAAGCACCGGCACA - 9600
9601 - GCATCAGCCCATGAGAGTGCTCCTGGCCTGAGAGGGTAAGGGTCAGGGCAGCTCAGGAGA - 9660
9661 - CCCTAGACCTGCATAGTGATCCCCCCACCAGGAAGGCCCCACAAGATGCTCACCTGCCCT - 9720

9721 - CCCTATCCCTGTCCCCAGCTGGAGGAGCACCGGAATTCACAGAAGCAGATGAAGCTCCTA - 9780
     -                   L  E  E  H  R  N  S  Q  K  Q  M  K  L  L

9781 - CAGAAAAAGCAGAGCCAGCTGGTGCAAGAGAAGGACCACCTGCGCGGTGAGCACAGCAAG - 9840
     - Q  K  K  Q  S  Q  L  V  Q  E  K  D  H  L  R  G  E  H  S  K

9841 - GCCGTCCTGGCCCGCAGCAAGCTTGAGAGCCTATGCCGTGAGCTGCAGCGGCACAACCGC - 9900
     - A  V  L  A  R  S  K  L  E  S  L  C  R  E  L  Q  R  H  N  R

9901 - TCCCTCAAGGTAGGCCTGGGCCCCCTGGAACAGGTGACTCTGGTTTCCTTGACTTCCACT - 9960
     - S  L  K

9961 - TAATGTTTCTTTCATGGGCTTTCCTCTTAAAAAGTAGTGCAGGCTAGGGCCAGGCGCAGT - 10020
10021 - GGCACACATAAGTGATTAAAAATCTTCTGGCCACTAAAAAACAGAAATTAATTTTAGTAA - 10080
10081 - TATACTTAACCCAATATCCAAAACATTACAATTTCAACATGAAATCAGTGTAAAAAAGCA - 10140
10141 - AGGCTGGGTGTGGTGGCTCACACCTGTAATCCCAACACTTTGGGAGGCTGAGGTGGATGG - 10200
10201 - ATCACTTGAGGCCAGGAGTTTGAGACCAACCTGGTCAACGCAGTGAAACCCCATTCTACT - 10260
10261 - AAAAATACAAAAATTAGCCGAGTGTGCTGGCAAATGCCTATAATCCCAGCTACTCAGGTG - 10320
```

Fig. 24 (continued; 5/9)

```
10321 - GCTCAGGCATGAGAATTGCTTGCACCTGGGAGGCTGAGGTTGCAGTGAGCCGAGATTGCA - 10380
10381 - TCACTGCATTACAGCCTGGGCAACAGAGTGAGACTCAGTGTCCAAAAAAAAAAAAAAGTA - 10440
10441 - GTGCAGGCTTGTGGCATAGAAATACACTTTCTCAATAATGCCTTACGTTAAGAGAGTACT - 10500
10501 - GCTTGTAATCATTTGACATGTATTAGATAAGGTGAAGGATAAAGTACTAAGAGAATCCAT - 10560
10561 - AATGCACTGGCGTTAGTATTTCTCAATGAAATGACAGTCCCCTGGTAAGCGGAGGCCTGG - 10620
10621 - CTCTGACAAGCAGCTCTTGTCCCAGACGTTGGTCAGTCAGGAACCTGGGTCCTTCCCATG - 10680
10681 - TTCTGCTGCTTCTATGGTGAGGTCAGTCTGTGGTTACACCAAGTTTAAATACAGCCTTTT - 10740
10741 - AACTTTCTTTTTTATATGTAAAATCTTACATGTAGTTTTTAGAATGAAATTATTATACAT - 10800
10801 - GTACCATTTCATATCCTGTGCCTTTTTTTCACTTTACATAACATTTTTCCCTATCAGTAT - 10860
10861 - GTGTAGGGCTATCTTCTCATTATATGGATATATTATATCAGTGCCCTAGTTAAAGCATTT - 10920
10921 - TGGGGGTTGTTTACAATTTTTCATTATTACATATAGAACTATAGTGAAAATTCTTGTTAT - 10980
10981 - ATTTATCACTGGTCAGTTATATAGAACTTATCTGTAGGATAAGTCATGGAATTGAAATGG - 11040
11041 - CTAGGTCACAGTATATGCAGATTTTTCATTTTAATAGATTTTGCTGGATTGCCTTCCAGT - 11100
11101 - GAGGGGGCAGTGTGCCTTCCCCATCAAAAGTGTTGAGTGCCTAATTCTGCACAACTTTGC - 11160
11161 - AAACCCTGGGTGTTACTAAATTTTAACAGCTTGGTCTCTGGGGGTACAGAGGGGACAAAT - 11220
11221 - GCACATTAATCTGAAATCTGGAAGAATAGGCCTTAGGAGATCCGACTTGCTTCAGAATGG - 11280
11281 - CACTTAGCACTTACATGTGTGCATGTGTGCCTGCATTTTTTCTTCCTTTTTTTTTTTTTG - 11340
11341 - GGGACGGAGTCTTGCTCTGTGGCCCATCGCCCAGGCTGGAGTGCAGTGGCGCGATCATAG - 11400
11401 - CTCACCACAACCTCCGCCTCCCAGGTTCAAATGACTCCTCTGCCTCAGCCTCCCAAGCAG - 11460
11461 - CTGGGACCACAGGTGCACACCATCACGCCGGCTAATTTTTGTATTTTAGTAGAAACGGGG - 11520
11521 - TTTCACCATATTGGCCAGGCTGGTCTCAAACTCCTGACCTCGTGATCCGCCCACCTCAGC - 11580
11581 - CTCCCAAAGTGCTGGGATTACAGGCGTGAGCCACCGCGCCTGCCATGTGCCTGCATTTTT - 11640
11641 - CTAGGGGGAGAATCTCACTTGATGTCACCTGATATACAGAGGGGCCCATTGGAACCCGCA - 11700
11701 - TTGCACAACATCCTGGAGTCTGGCTACTCCACGCTTTGGGAGCAGGGAGGGCTGTTGGCA - 11760
11761 - GAGACCATCTGTGGACTAGCTGGGGGACCCTTGTGAGGTAGCAGTGGATGATGGCTCTCG - 11820

11821 - GGCTGACTTCTTTGCCCAGGAAGAAGGTGTGCAGCGGGCCCGGGAGGAGGAGGAGAAGCG - 11880
      -                     E  E  G  V  Q  R  A  R  E  E  E  E  K  R

11881 - CAAGGAGGTGACCTCGCACTTCCAGGTGACACTGAATGACATTCAGCTGCAGATGGAACA - 11940
      -  K  E  V  T  S  H  F  Q  V  T  L  N  D  I  Q  L  Q  M  E  Q

11941 - GCACAATGAGCGCAACTCCAAGCTGCGCCAAGAGAACATGGAGCTGGCTGAGAGGCTCAA - 12000
      -  H  N  E  R  N  S  K  L  R  Q  E  N  M  E  L  A  E  R  L  K

12001 - GAAGCTGATTGAGCAGTATGAGCTGCGCGAGGAGGTAAGGGTATCACGGACAGCAGTCAT - 12060
      -  K  L  I  E  Q  Y  E  L  R  E  E

12061 - GGCCCAGAAATTGTGAGGTTTTGAGTGTGTGCTAGGCACTGGGACAGTACCTTTTCAGGC - 12120
12121 - TTCATCCCATTCTCCCTTTCTTCCTCCTCCTCCTCCTTGGGAGGAGAGTAATGTTATTCC - 12180
12181 - TCATAGATAAAAAACAGGTGTGGAGAAGAGACTCACTTACAGCCACACAGCCCCAGGTCC - 12240
12241 - ACAGTGCCTTGTCCCAAATGACTGGGCCAGGCATCTTTTGGAATTAGAACTATCCACATT - 12300
12301 - TTAGAATGGAGGTACATGTATGGACTGTGTGTTATATAGCACCCTCAGCAGGGCCTTGGG - 12360
12361 - GAAGCCAGACACATTAATGTATTTATGCAGTAGAACTTCCAAATACTCACCTACATTATG - 12420
12421 - GGCTTACAATGATGCAGGTCAAGTCTGGCTGCCAGCTTATGACAATTTCCATTTTCAGAA - 12480
12481 - CTTTGTAGAATTTGGAATTGCAGGGGAGGGGTGTACCTGTGATCAGTGATGGACTCCAGA - 12540
12541 - GACTGTGTCCACTGATTCCTTGCTGCTCCTGCCACTCAAAAGGCAGAATTTATCAGGCTG - 12600
12601 - GGCGTGGTGGCTCATGCCTGTAATCCCAACACTTTGGGAGGCCAAAGCGGGCGGATCACC - 12660
12661 - TGAGGTCAGGAGTTCAAGACCAGCCTGGCCAACATGGTGAAACCCTGTCTCTACTAAAAA - 12720
12721 - TACAAAAAATTAGCCAGGTGTGGTGGTGCACGGCTGTAGTCCCAGCTACTCAGGAGGCTG - 12780
12781 - AGGCAGGAGAATTGCTTGAACCCAGGAGGCAGAGGTTGCAATGAGCCAAGATTGTGCTAC - 12840
12841 - TGCACTCTAGCCTGGGTGATATACCGAGACTCCATCTCAAAAAAAAAAAAAAAAAAAGC - 12900
12901 - AGGATGTCACTCCCTTTGTCACTGCGTTGGCTGCCACCCCAGGCACTTGAATCTTTGGAT - 12960
```

Fig. 24 (continued; 6/9)

```
12961 - CTTCCCTGCCAGTCACCTGGCTGTTCTGGGCGCGTTCTCATCATGAGAAGGGAGACCTGC - 13020
13021 - AGCCCCCTTACAGGGCTGGCAGAGGACCTGCTCTGGATTAGGCCCTTTCCTAGCCCCTGG - 13080
13081 - GGTGTGGCAGTGGGTGAGACCGGGAAGATCTGCCCTCTTAGGTTCATAGGCCAAAGTGAT - 13140
13141 - GATCGTGTGTGCAGGACCTAGAGGGCGCTCCCCTGACCCACCCCTTTCCTTGCCATACTT - 13200
13201 - CATCCTCTGGGAACAAAGCTGCTTGTTTGGTTTGAGGGGAGTTGGTTTGGTTCTTATCCC - 13260
13261 - TCAGCGCTGAGACATAGAGGCTTCCTGGGCCACTACAGTGAGACACGAACTTCAAGAATC - 13320
13321 - TGAATACCCCCGTTTTCTCTCCCCGCCAAGGCAAAAAAGGACTTAGTACTACCTGTGGAG - 13380
13381 - AAGGAGGTGCAGGACTACCAGGCCCTGCTGCTTTGCATTTACAGCCCTCCCCAGACAGAC - 13440
13441 - ACAGGCACCCTCATCATACCCAAACTGGACTTACCTGCTAGGCACCTTCCCTTCCCCATC - 13500
13501 - CAAAAAAATGGAGTTATTTTCCCTTATTTCAGCAAGTCCAGTTGATTTTACCTTTGAAGT - 13560
13561 - AGCACCTGAGTCCTTCACCTTCTCTCCATCCCTTCTCTCTCACCTGACACAGGTCTGCAG - 13620
13621 - CGCTCCTCTAGTAGGCAGGACAGCCATTCCTTGGGGATGCACATGTCTAGTCTTTGCCTA - 13680
13681 - GATATGGCAAGTCTTTGCCAACTGAGCTAGGCTGTTATGTTCTTAGAGGCATTGTTTTTG - 13740
13741 - CCCATTCTTCCCATTTACAAGAGAATCAGGGACACAGAAGTGAGGGCTTCCAGCCCCATA - 13800
13801 - GGTGATCAATCCTGGGGTCAGAGATTTGAGTGTGTTTATTGCTTGCCTTCTTGGGAGCAG - 13860
13861 - ATTCCATCCATAAACCATGTGCTTACCAAGGTCTGACTCACTGGGAGAGAAACGACGTGA - 13920
13921 - GGTTGGAAAGCTGACCTTCCAGAGACTTGGGGCCCATGTTGTGTGGTACACATGGGAGTC - 13980
13981 - CATCATATCAGATTGAGATGGGGGGCTGGGCAAAGTGCCCTGGTCTGTGGCTGTGGGGCT - 14040

14041 - ACCCTGAGAAAGGGAGCGCCTGACAAGCCGACTGCTCCCACCATCTTTGTTGCAGCATAT - 14100
      -                                                       H  I

14101 - CGACAAAGTCTTCAAACACAAGGACCTACAACAGCAGCTGGTGGATGCCAAGCTCCAGCA - 14160
      -  D  K  V  F  K  H  K  D  L  Q  Q  Q  L  V  D  A  K  L  Q  Q

14161 - GGCCCAGGAGATGCTAAAGGAGGCAGAAGAGCGGCACCAGCGGGAGAAGGATTTTGTGAG - 14220
      -  A  Q  E  M  L  K  E  A  E  E  R  H  Q  R  E  K  D  F

14221 - GCTCAGGCCCCAGGGTTGGGGTGGGGGTGTGGGAGGAGACAGGCTGGGCTCTGGCTCAGC - 14280
14281 - TCATAGCCGGGTTATATGGGAGAAGTCTGGCCAGACCAGGCACAGATTCCTTGAGTACCA - 14340
14341 - GTCTGAGAGCAGGAAGCCTCAGTGGGTCTGGTGCTTGTGGCTAAAAACCAAACATAGCCC - 14400

14401 - CTGGGGGCTTCTGACAGGATCTGGGGTTCTGTCTTGGAAATAGCTCCTGAAAGAGGCAGT - 14460
      -                                                 L  L  K  E  A  V

14461 - AGAGTCCCAGAGGATGTGTGAGCTGATGAAGCAGCAAGAGACCCACCTGAAGCAACAGGT - 14520
      -  E  S  Q  R  M  C  E  L  M  K  Q  Q  E  T  H  L  K  Q  Q

14521 - GAGAGCATATAACCTGACCCTGTGCCTTCAAGTTTCCCTCACTGGGCCCCATCCTGGGGG - 14580
14581 - TAGTGAAATGGGACCCTCATTCTAGGACTGGCTGTGTCCTGGCTGCTATGACGCCTTGGT - 14640
14641 - TGAGCTTAGGTGGGCTCAGAGGACTTCATTTGTAGCTCAGAAATGTATTGCTTTTGAGGA - 14700
14701 - GGTAGGAACAGAAGAGTTTGAAAATCAACATAAAGGCAAAATAAAAGTCACCCTAAGTCT - 14760
14761 - CCTACTTTCCAGGCTTAGCATTTTGGATTATATCCTTCCAAATATATAGCTTTGCTTTGT - 14820
14821 - TTTAAGGAAAAATAGTATCTCAATAGAATTACTGGTCAGAGAGTCAAGGACGGGTCTGAG - 14880
14881 - TGTGTTGACCAGAGTGCCTCCCAGAGAAACCCAGTCTTATCTGTGGGCTGCTTTCTCCCC - 14940

14941 - ACAGCTTGCCCTATACACAGAGAAGTTTGAGGAGTTCCAGAACACACTTTCCAAAAGCAG - 15000
      -     L  A  L  Y  T  E  K  F  E  E  F  Q  N  T  L  S  K  S  S
```

Fig. 24 (continued; 7/9)

```
15001 - CGAGGTATTCACCACATTCAAGCAGGAGATGGAAAAGGTAACTGTGGTCCAGGCCAGGCA - 15060
      -  E  V  F  T  T  F  K  Q  E  M  E  K

15061 - TGGCTGCTGGGGCATAAGCTGCTTCATTCAAAATTGTTGGGCCTGCCTTCAGGAAGCTCC - 15120
15121 - CATCTGGGGTGTCTCAAGGGCAGGGCTGTTAGGAAGGTTCACAGCCTTTCCCCTCTTGAG - 15180
15181 - GCAGTATCAGTGGTATGTATACACTCCAGGTTGTCCCAGGGAATGGGGCAGTCTTTTCTG - 15240
15241 - TTTGTTTGGTTTTTTTGGGGGGTTTGTTGTTGTTGTTGTTGTTGTTGTTTGAGA - 15300
15301 - TGGAGACTCACCTATTGCCCAGGCTGGAGTGCAGTGGCATGATCTCAGCTCATTGCAGCC - 15360
15361 - TTTGCCCCCCGGGTTCAAGTGATTCTCCTGCCTCAGCCTCCTGACTAGCTGGAATTACAG - 15420
15421 - GCGCGTGCCACCATGCCTGGCTAATTTTTTCTTTCTTTTTTTTTTGTATTTTTAGTAGAG - 15480
15481 - ACGGGGTTTCACCATGTTGGCCAGGCTGGTCTCGAACTCTTGGCCTCAAGTGATCTGCCC - 15540
15541 - GCCTTGGCCTCCCAAAGTGCTGGGATTATAGGCGTGAGCCACCATGCCTGGCCCCTTACC - 15600
15601 - ATTCCTTGTTATTGGTGGTGGACACCTCTGACTTCCTGGTGGTGAGGTGGCACAGAGGGC - 15660
15661 - ATTGACTGCATCCTGTAATGCCTTGCGCCTTGGGATCAATCATTCCCCACCTTGGAGACA - 15720
15721 - CAGGTGCAGTCCCCACCTTGGAGACACAGACCTTGGAGAGGCCAGCTCTGACCATTTCCT - 15780

15781 - TCTGTCTGTCACATAACCTAGATGACTAAGAAGATCAAGAAGCTGGAGAAAGAAACCACC - 15840
      -                      M  T  K  K  I  K  K  L  E  K  E  T  T

15841 - ATGTACCGGTCCCGGTGGGAGAGCAGCAACAAGGCCCTGCTTGAGATGGCTGAGGAGGTGG - 15901
      - M  Y  R  S  R  W  E  S  S  N  K  A  L  L  E  M  A  E  E

15902 - GCTGTCTGTGATCTGCAGCCAGGGTGGGGGTGTGCACTTAGCGCATATCAGGCCCTTTCC - 15961
15962 - TGTATGTTCTACCCATCAGTGACACAGCTAGCATGAGGTAGAGGTGAGATTTGCACACAA - 16021
16022 - TGTCCAAGTCCAAAGTTAATGCTGTTCTCTCCCCATGGGAGGTGGTGAGCCCAGTGGTAG - 16081
16082 - GTCTCCAGTGGGAGTGAAGGGAGCAAATGGAAGAAAGGAATAAAAGAGCAGAAAAAAACG - 16141
16142 - GGTGCCAGTGATGTGCCTGGTTTACATGTAAAGCAGCCCAGGTAGTTTGTGATTTCACAG - 16201
16202 - CTTGTAATGTAGAAGAAAGGAACTAACGATGGAGCAGCAACTGCAAGCCAGACCTTGCTG - 16261
16262 - AAAGTTTTTGGGTTTTTTTTGTCTTTTTTGCTGCTGAATGTTTTTAGGTACGTTGTTCAT - 16321
16322 - TGAACCTTCTCTTGAGCTCTGAGGATGGTATTAGTAGTCCTGTTTTATAGATGAGACAGG - 16381
16382 - CTCAAAAGTCAAGTCCTTTGCCAAGGTCACGTGGTAGATAAATGGAGGAATACGTTATCT - 16441
16442 - CCAAGCCGTGCCCCTTTTCTGCACCATGCTGCCCCACCTGACAGCCTAGTCATGGCTTCA - 16501
16502 - ACTAGGACTGTTTCCTAAAGGGGGCCAGCTTTGGACTCGGTCTGCTCTCAGCCTTGTTAA - 16561
16562 - AGTGTTTGCCGCCAAGTGGTGATGGTAAGTGGGAGGTTGATGGGGCACGGCACTGAAGGT - 16621

16622 - CTCATTTCTTTCCCTAGAAAACAGTCCGGGATAAAGAACTGGAGGGCCTGCAGGTAAAAA - 16681
      -                  K  T  V  R  D  K  E  L  E  G  L  Q  V  K  I

16682 - TCCAACGGCTGGAGAAGCTGTGCCGGGCACTGCAGACAGAGCGCAATGACCTGAACAAGA - 16741
      -  Q  R  L  E  K  L  C  R  A  L  Q  T  E  R  N  D  L  N  K  R

16742 - GGGTACAGGACCTGAGTGCTGGTGGCCAGGGCTCCCTCACTGACAGTGGCCCTGAGAGGA - 16801
      -  V  Q  D  L  S  A  G  G  Q  G  S  L  T  D  S  G  P  E  R  R

16802 - GGCCAGAGGGGCCTGGGGCTCAAGCACCCAGCTCCCCCAGGGTCACAGAAGCGCCTTGCT - 16861
      -  P  E  G  P  G  A  Q  A  P  S  S  P  R  V  T  E  A  P  C  Y

16862 - ACCCAGGAGCACCGAGCACAGAAGCATCAGGCCAGACTGGGCCTCAAGAGCCCACCTCCG - 16921
      -  P  G  A  P  S  T  E  A  S  G  Q  T  G  P  Q  E  P  T  S  A

16922 - CCAGGGCCTAGAGAGCCTGGTGTTGGGTCATGCTGGGAAGGGAGCGGCAGCCCAGCCAGG - 16981
      -  R  A  *
```

Fig. 24 (continued; 8/9)

16982 - CCTGGCCCATAAAAGGCTCCCATGCTGAGCAGCCCATTGCTGAAGCCAGGATGTTCTGAC - 17041
17042 - CTGGCTGGCATCTGGCACTTGCAATTTTGGATTTTGTGGGTCAGTTTTACGTACATAGGG - 17101
17102 - CATTTTGCAAGGCCTTGCAAATGCATTTATACCTGTAAGTGTACAGTGGGCTTGCATTGG - 17161
17162 - GGATGGGGGTGTGTACAGATGAAGTCAGTGGCTTGTCTGTGAGCTGAAGAGTCTTGAGAG - 17221
17222 - GGGCTGTCATCTGTAGCTGCCATCACAGTGAGTTGGCAGAAGTGACTTGAGCATTTCTCT - 17281
17282 - GTCTGATTTGAGGCTCAGACCCCTCCCTGCCCTTCAGAGCTCAAGACAAGTAATACACCC - 17341
17342 - AGGTCTTGACTGCATTTGTCTTGTGAGCAGGGCTTGCTTGGTCAGCTCAGGCCCTCCTAG - 17401
17402 - CTGCTCTGGAGGCTCCTTTGATTCTCTAGACCTGGAAAAGGTGTCCCTAGGCAGAGCCCT - 17461
17462 - GGCAGGGCGCTCAGAGCTGGGGATTTGCTGCCTGGAACAAGGGACCTGGAGAATGTTTTT - 17521
17522 - GCGTGGGATGATGTGCTGGTCAGGAGCCCCTTGGGCATCGCTTCCCCTGCCCTTTGGTAG - 17581
17582 - TGCCAGGACCAGGCCAATGATGCTTCTCAGTAGCCTTATCATTCACAGGTGCCTCTCTAG - 17641
17642 - CCTGCACAAATGATTGACAAGAGATCACCCAAAGGATTATTTCTGAAGGTGTTTTTTTCT - 17701
17702 - TTATTTCTTTTTCTTTTTTTTTTTTTTCTTTTTCTTTTTTTTTTGCACATGACAGTGTT - 17761
17762 - TGTATTGAGGACCTTCCAAGGAAGAGGGATGCTGTAGCAGTGGTGCCTGGGTGCCTGGCC - 17821
17822 - TCCAGTGTCCCACCTCCTTCACCACCCCACTTGGCTCCTTTGCCATCTTGATGCTGAGGT - 17881
17882 - TTCCTGTTTGGTGAGATCAGGTTGTTTGTGGTAAAAGAAAGGAAAGGGCTTCTGATGGCT - 17941
17942 - TTGCCACAAGCTTACCTGTGGGTTTCAGTCCTGAGAGGCCACCACCAGTTCCCATCAGCA - 18001
18002 - CTGTCTCCATGCAGCAGTTGCTGGGTCCCATGTCCAGCTGCCTCTTTGGCTTCATGGGTT - 18061
18062 - TTTCTGCTTCCTGCCCCCACCCCCACATGTGCAATCCTCAAGATTTGTCCTGATTCTATT - 18121
18122 - TCCTGGCACCTCCCTGCCTGTCCTTGGGGATTCTACTTCTTCCTGTGTGGGAGCCCATAG - 18181
18182 - CTGTTGTCTAACAGGTAAGAAATGAAATTGAACTATTGACTGGGCCCCAGAAATCCATAA - 18241
18242 - AATGGCTGCAGACAGTTGTTTCTGTGTCCTGTTCTACCCCCACTCCAGTACATAACTACT - 18301
18302 - ATGTACTGTGTAGAGCCATTCTATATGCTGAATGTTCTGCTGTTGCAAACTTGCCAGGGT - 18361
18362 - ATTAGCCAGTGTTTGTGCCAAGCAGTTTTCTGGGACAACAGAATGACTCAGACCAAGATG - 18421
18422 - GATAGGATGGTTAGGGCTTTGCTTCTTGCTGTTTTTCTTTGAAGCTAGTTCATTGTCCTG - 18481
18482 - CAGGTCCCTTCATCTTCCATACCTAGCCCACTCTTTTAGCCCTTACCTTAAATCTCTCAG - 18541
18542 - ATAAGTTGGTTCACAAAGAATGTTAAGTACTGAATCATGTGTGACTGAGACCAGAGATGG - 18601
18602 - CAAATGAATGGCACACCATTTCTCCTTCTCCTGCCCCAGGGCAGGTACCACTGATCTGCA - 18661
18662 - TCAGAGTTGCCTGCTATTCTCTGGTGTATCCTTCACATCTAGGTGCCCTCAAGCAGCTGT - 18721
18722 - GTGAGTGTTGAGATCTCTGCCATCTCTGGCTGAGATACTGCTGTCCTGTGAAGTGTTTCC - 18781
18782 - CATGACCTTTTTCTTCCCCTTTGAATCCCTCTGTCTGGAGTAGTCCTTGCCTCTTCCTGC - 18841
18842 - TCCAGTAGGGCCTTTTCCCTACCCCAGCCCCTGTGCCAGGCTAAGCTGGTACAAGAGCTG - 18901
18902 - CCAACCTCACAGAGTGTTTGCTAGGCGAGAGAGGTGCAGGGAAGAGGCAGAGGTATGCAC - 18961
18962 - CTTCCCCCTTGAAGAGAGGGGAAAGGCCTACAGTGGCCCACATAATTGCCTGACTCACAC - 19021
19022 - TTCAGCTACCTCTTAATGCCTGTGGAGGGACTGGAGCTGCTGGATCCCAGTGTGGTGGTG - 19081
19082 - TAGGAGGCCACAGTGAGCAGGTGGCCCCAGCTGGGTTTCCCAGGTCAGGAATGTGGGCCC - 19141
19142 - CAGGCAAGGTGCAGCCTTTGCTCACAGCTCCATCCATGTCTAGACCTTCAGGCCAGTCTG - 19201
19202 - CAGATGAGGTTCCCTACCTTTTTCTTCTCTTCATTGACCAAATCAACCAATCACTACAGC - 19261
19262 - TGCTCTGCTTCTGCTTTCCAAAGTAGCCCAGGTCCTGGGCCAGATGCAGGGGAGGTGCCT - 19321
19322 - ATCCATGAGTGAAGGCCAGTGTCTTCCTCACCTGGGTGGGTCCCACACTTGTGACCTCAG - 19381
19382 - TTTTAGGACCAAGATCTGTGTTGGTTTCTTAGATTGCTAGCTTTTCCTCCAGGGGACCAC - 19441
19442 - AGCAGGTGAAGCTCAAGAGCGCATGGCTCTGCTAATAGTAAATTGTTTTCAGGGCCTTGT - 19501
19502 - CCAGCTGAGAGCTTCATGTCCACCAGATTCTGAGAGGTGTCAGCAGCACTTTTTTTTTTT - 19561
19562 - ATTTGTTGTTTGTTTTCCATGAGGTTATCGGACCATGGGCTGAGCTCAGGCACTTTCTGT - 19621
19622 - AGGAGACTGTTATTTCTGTAAAGATGGTTATTTAACCCTTCTCACCCCATCACGGTGGCC - 19681
19682 - CTGAGGGCTGACCCGGAGGCCAGTGGAGCTGCCTGGTGTCCACGGGGGAGGGCCAAGGCC - 19741
19742 - TGCTGAGCTGATTCTCCAGCTGCTGCCCCAGCCTTTCCGCCTTGCACAGCACAGAGGTGG - 19801
19802 - TCACCCCAGGGACAGCCAGGCACCTGCTCCTCTTGCCCTTCCTGGGGGAAGGGAGCTGCC - 19861
19862 - TTCTGTCCCTGTAACTGCTTTCCTTATGGCCCAGCCCGGCCACTCAGACTTGTTTGAAGC - 19921
19922 - TGCACTGGCAGCTTTTTTGTCTCCTTTGGGTATTCACAACAGCCAGGGACTTGATTTTGA - 19981
19982 - TGTATTTTAAACCACATTAAATAAAGAGTCTGTTGCCTTACTTGTTTCTCTCCTGACCTG - 20041
20042 - TGTATTCCTTTGTTTCTGGATCTGATCCATTCAGCCCCTTCCATCATCACTGACTTGTTC - 20101
20102 - AGGTCTGCTGCAGAGCGCCCATGGTGGTTCCCTGGTATCTTACATATTCCACAGTGTCTT - 20161
20162 - TGAGCAGTCGCCACAGCCTCAGGATGCTGGCATATTCACTTGAGCTGCCTGAGTGGAGCC - 20221
20222 - CTTGGCAAAGTTGGCAAGACCCTTGCCTCAGAGAGGATCACACACACACAAAAAAGTTTT - 20281

Fig. 24 (continued; 9/9)

20282 - CCCTGACCTGGGGGCTCACAGGCTAGTGAAGGGAAAAGGTACTTTTAGCTATAGACAGGT - 20341
20342 - CAATGGTGCTGAGAGCAGAGAGGAGGCCCCTGCCCCCTTCAGCAAGGTGAGGGGTGATA - 20401
20402 - CCTGGAATGGCCTTCTGAACCACAGGGCAGGTAGAAGATGAACGTCATTTAGTGATTAAA - 20461
20462 - TGGTACAGCTGGGAAGCAGGTCCATGGGACTGGGAGAGGGGGTGAGGCTGGGCCCAGAGT - 20521
20522 - CTGGGTACCAGGTTAAGGAATGTGGGCTAGATCCAGAGGGCAGGGGGGGCAACTGAAGGT - 20581
20582 - GTTTCAATAGGAAATTGATAGGCTCCAGCAGTAAGGCAAAAGGCATGGAGCCAGGCATAG - 20641
20642 - GCCATTTGAGGCCCAGGTTAAGAGGGGTGGACACTCATCACTGCTATTTGGGTCTGAGCT - 20701
20702 - GTGGGTAGGCTCCTATAGCCCTGGCCTGCCCAAGGGAATTCACAGGGGCCTCTAATTGTA - 20761
20762 - TGCATTCCTTAAGGAGAGCACATTCTCTGTTCAGTTTTTACACCCCCCATTTACCCACCT - 20821
20822 - CAAGCATGGGACTCCTATATGGGAGACATGCTGCTGGTGGCCTCACCCAGCACCCTGTTC - 20881
20882 - TCTCTGGGTCCTGGGTTGGTCAGGCACAAAGGATGATATGTGCTGAATGCCCAGGAAATG - 20941
20942 - GCAGAGACAACCCACCTGCCCTTCCCTCCAGGCCTCCACAAATAGATGTGCCCACAATGA - 21001
21002 - CTGTGACAGTCCCAGCAGAGCCTCTGACCCTTCTAGCTGGGTCCTGATACATGTTTTCCA - 21061
21062 - TGCTGGCCATGTTATTTCTAGTCGCAGATCCTCTGGAGGGTGTGGGGGGGGTGCCGCCCC - 21121
21122 - AACTCTTGGAGATTCCAAGCAAAGCAGCTCTGAGAATAATGAGGTTTCTGACCCCCCAGT - 21181
21182 - GAAGCAGCTGAGGATGGGAACCACAGGGGTGCTCCCTCTGTCAGCAGCATTACCACTGTC - 21241
21242 - TACTCTAGCAGCTCCGGTGGGGAAGGAGAGGGATTTCTGTTGTCCCCAGTCTGGGCCCCT - 21301
21302 - GGTTATTGAAAAAGTTCGGAATTACTCTTTACCCTTGTGGAGTGTTCTGAGTGTTGGAAG - 21361
21362 - TACCCAGGAAGAAGCCCTGAGCAGGTGCCCTCAGGAGCAGTGCCCATGGCTCCCCACATC - 21421
21422 - AGCCAAGAGGCCCAACCCCAGGAAGCCACTCCTGCCCGGGGATGGGGAAGGTGGGCTGGG - 21481
21482 - TGGCTGTGTGCACTGCCCTGGGCCAGCTCACTTGAGCCTGCTGAGCCGCCTGGCCAAACA - 21541
21542 - TGAGCCTCTCTCCTGTTGTATCAGATGCTGTTCTGGGGACCTGCGCCAGGAGCCTCTGCC - 21601
21602 - AGGGCTTTAAATAGCTGCCCCCATTGATCTGGCTGCAGGCAGCAGCAGTCACACTGGGTC - 21661
21662 - AGCCTCCATCAGGTGCTCAGGTTTCCCTGAGGACTGGAGTCAGGTGCCAGGGAATCGCGT - 21721
21722 - GGTCTACCTTATGACCTGGTGCTCCCCACACCTGTCTCCTAGGCCTGGGGGGTGGGGAGG - 21781
21782 - ACTCCTGTCACTTCATCTGCGGCAAAATACAGCCCCCACCACTTACCAGAGAAAACTGTC - 21841
21842 - TGGCATTGTAGAGAGAGGGGTTTTGCCCTCAAAAGACTGTTGCTTACTTTCAGTAGAATG - 21901
21902 - GGGAATGACACTGGTATCTTCCTTAAGGGTTGTTATGGGGATGAAATGTATGTAAAGTGC - 21961
21962 - TCAATAGGGCACTGGACTCACTCCATTGATGGCTGTCTTTGCTCGAAGTGTCTTCCTGAT - 22021
22022 - GCTGCTGCTGTTGCTGCTTGTGCTTCTTCTGTGCTTACATTCTCTCTCTCTCACTCACTC - 22081
22082 - ACTCTGTCTCTCCTCTCCCCCGCCCCACCCCCTTTCTGACAAAGCCACCACCATTTTGTA - 22141
22142 - AGGAACTGTAGCTTCTCTCTGAAACTGCCGGGAAAGGGAAAATCTTTTTAAAATAGACAT - 22201
22202 - CACACAACCAACAGGGTCCCCTAGGTTCAGGCGGGGAGGTGAGGTCGAGTGAGA - 22255